

genCore version 4.5
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OM protein - protein search, using sw model

Run on:

June 18, 2002, 17:42:59 ; Search time 34.93 Seconds
(without alignments)

2314.965 Million cell updates/sec

Title: US-09-423-516-2
Perfect score: 4126
Sequence: 1 MWVTKLIPALLQHVLHL.....VAYYAKWIKIILTYKVPOS 728
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574
Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Genesed_032802:*

1: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1980.DAT:*

2: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1991.DAT:*

3: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1982.DAT:*

4: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1983.DAT:*

5: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1984.DAT:*

6: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1985.DAT:*

7: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1986.DAT:*

8: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1987.DAT:*

9: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1988.DAT:*

10: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1989.DAT:*

11: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1990.DAT:*

12: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1991.DAT:*

13: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1992.DAT:*

14: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1993.DAT:*

15: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1994.DAT:*

16: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1995.DAT:*

17: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1996.DAT:*

18: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1997.DAT:*

19: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1998.DAT:*

20: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ1999.DAT:*

21: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ2000.DAT:*

22: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AJ2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID
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Description			
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1	4126	100.0	728 14 AAR42062
2	4126	100.0	728 17 AAW00338
3	4126	100.0	728 17 AAW00340
4	4126	100.0	728 19 AAW59022
5	4126	100.0	728 19 AAW58096
6	4126	100.0	728 19 AAW42996
7	4126	100.0	728 19 AAW39207
8	4120	99.9	728 14 AAR39321
9	4119	99.8	728 13 AAR25176
10	4119	99.8	728 14 AAR40862
11	4118	99.8	728 13 AAR20005

ALIGNMENTS

RESULT ID	1
AAR42062	standard; Protein: 728 AA.
XX	
AC	AAR42062;
XX	

DT 15-NOV-1993 (first entry)

DE	Vascular endothelial cell growth enhancer protein.
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XX	Enhance; growth; vascular endothelial cell; human; tumour; cell line;
KW	HUOCA-II; HUOCA-III; blood vessel; wounds; burns; decubitus;
KW	post-operative tissue damage; drug; cardiac angiopathy.

OS	Human sapiens.
XX	
PN	EP550296-A.
XX	
PD	07-JUL-1993.
XX	
PF	27-NOV-1992; 92EP-0403199.
XX	
PR	28-NOV-1991; 91JP-0337999.
XX	
PA	(TERUMO) TERUMO CORP.
XX	
PI	Adachi M, Harada K, Hirahara I, Sudo T;
XX	
DR	WPI; 1993-215669/27.
DR	N-PSDB; AAQ45702.
XX	
PT	Vascular endothelial cell growth factor protein - used for promoting angiogenesis in the treatment of cardiac angiopathy,
PT	wounds, burn injuries, postoperative tissue damage etc.

Human hepatocyte g

12	4116	99.8	728 20 AAW88529
13	4115	99.7	727 12 AAW10656
14	4113	99.7	728 12 Human hepatocyte g
15	4112	99.7	728 12 Human leukocyte-de
16	4112	99.7	728 20 AAW88531
17	4111	99.6	728 20 Human hepatocyte g
18	4110	99.6	728 17 AAR87525
19	4109	99.6	728 17 AAR87523
20	4108	99.6	728 14 AAR40863
21	4107	99.5	728 12 AAR14243
22	4106	99.5	728 17 AAR87524
23	4096	99.3	728 15 AAR47227
24	4095	99.2	728 17 AAR87522
25	4088.5	99.1	723 11 AAR07144
26	4088.5	99.1	723 12 AAR15624
27	4088.5	99.1	723 15 AAR57028
28	4088.5	98.9	723 13 AAR25577
29	4088.5	99.1	723 19 AAW76690
30	4085.5	99.0	723 13 AAR21142
31	4085.5	99.0	723 15 AAR57027
32	4085.5	99.0	723 15 AAR57028
33	4081.5	98.9	723 13 AAR25577
34	4077.5	98.8	723 19 AAW59193
35	4073	98.7	728 13 AAR25160
36	4066	98.5	728 12 AAR12792
37	4066	98.5	728 19 AAW48221
38	4066	98.5	728 20 AAW97041
39	4066	98.5	728 22 AAG68090
40	4066	98.5	728 22 AAB84517
41	4064.5	98.5	723 13 AAR29199
42	4064.5	98.5	723 17 AAR99588
43	4064.5	98.5	723 17 AAR99689
44	4061	98.4	728 13 AAR21976
45	4061	98.4	728 14 AAR52942

Human hepatocyte g
Hepatic parenchyma
Human hepatocyte g
Human hepatocyte g
Human hepatocyte g
Mutant hepatocyte
Mutant hepatocyte
Competitive inhibi
Human hepatocyte g
Mutant hepatocyte
Hepatocyte growth
Mutant hepatocyte
Tumour cytotoxic f
Human modified tum
Recombinant human
Tumour cytotoxic f
Human Leukocyte-de
Human hepatocyte g
Human hepatocyte g
Human hepatocyte g
TCF-II. AAR29199
TCF mutant having
TCF mutant having
Human Hepatocyte g
Human hepatocyte g

PS	Claim 5; Page 18-21; 44pp; English.
CC	This sequence represents a single chain protein which selectively enhances the growth of vascular endothelial cells. This protein was produced by the human tumour cell line HUCCA-II or HUCCA-III. This protein enhances the formation of new blood vessels and may be used to enhance healing of wounds, burns injuries, decubitus or post-operative tissue damage. It may also be used as a drug for cardiac angiopathy.
CC	used to enhance healing of wounds, burns injuries, decubitus or post-operative tissue damage. It may also be used as a drug for cardiac angiopathy.
XX	sequence 728 AA;
SQ	<p>Query Match 100 %; Score 4126; DB 14; Length 728; Best Local Similarity 100 %; Pred. No. 9.5e-277; Indels 0; Gaps 0; Matches 728; Conservative 0; Mismatches 0;</p> <p>QY 1 MWVTKLPAULLQHVLHLLPLTAIPAYAEGQRKRNTIHEFKSAKTLIKIDPALKIK 60 1 mwvtkilpalilqlvhvihllplaiyaaegqrkrntihfksaktlidpalkik 60 61 TKKVNADOCANCRTRNKGKLPFTCKAKFVKDARKOCLWFPPNSMSGVKEFGHEDLYE 120 61 tkkvnadqganrcntrnkgkpfckafvfarkqklwfpsmsggvkfkgfhefdlye 120 QY 121 NKDYIRNCITGKGSKYKGTVTSKSGKICOPWSSMIPHESFLPSYRGKQLOQENYCRNP 180 121 nkdylircnclgkgrsykgtvtsksgkicopwssmiphensfipssyrgkqloqenycrnp 180 181 RGEEGGPWCTTSNPVEYEVCDIOPCSEVEMTCNGESYRQLMDRHESGKICQRMWDHQTP 240 181 rgeeggpwcttsnpvevcdipqcsevemtcngesygldhtesgkicqrvdqhtp 240 Db 241 HRHKFLPERVPDKGFENDNYCRNPDPQGPPRPMCYTLDQHTRWEYCAIKTCADNMNDTDVPL 300 QY 241 hrhkflpervpdkgfendnycrnpdpqgpprmpcytldqhtwreycaktcadnmndtdvpl 300 Db 241 hrhkflpervpdkgfndnycrnpdpqgpprmpcytldqhtwreycaktcadnmndtdvpl 300 QY 301 ETTECIOQDGEGYRGTVNTIWGICPQQRWQSOPHYRHMMPENFKCDLRENYCRNPDS 360 301 etteciqdgqegyrgtvntiwigicpqqrwqsophyrhmmpenfkcdlrenycrnpds 360 361 ESPWCETDDNIRVGCSQTPNCMDSHGQDGCRGNGKNYMGNLSQTRSGLTCMSWDKNAME 420 361 espwcetddnirvgcsqtpncmdshgqdgcrgnknymgnlsqtrsgrltcsmwdkname 420 Db 421 DLHRHITFWEPASKLNEYCNRPDDAHAHPWCYTGPNLPIWPCPTSRCGEDTTPTVNL 480 QY 421 dlhrhitfwepasklneycnrpddahhpwcytgpnlpwpcptsrcgedttptvnl 480 421 dhrhitfwepasklneycnrpddahhpwcytgpnlpwpcptsrcgedttptvnl 480 481 DHPVTCASKTQKOLRVUNGIPTRNTGWMVSRLYRNHICGSLIKESWLTAQCPSPRD 540 481 dhpviscaktqkolvungiptrntgwmvsrlynhicslikewsltaqcpisrd 540 Db 541 LKDYEARLGHDVHGRGDECKQKQVLAVSQLVYGPESGLVLMKLARPAVLDFFVSTIDLP 600 QY 541 lkdyearlgdvhgrgdekkqvlavsqlvygpessglvlmklarpavidffstidlp 600 Db 541 lkdyearlgdvhgrgdekkqvlavsqlvygpessglvlmklarpavidffstidlp 600 QY 601 NYGCTTPEKFTSCSVYWGTYGSLINYVGYLRYAHLYINGNEKCSQHHRKGKVTLNESETAG 660 Db 601 nygttpekftscsvywgtygslinyvgylyahlyingneksqhhrkgkvtnleseitcg 660 661 AEKIGSGPCGCGYGGPLVCEQHMKMVLGLVIVPGRCALIPNRGIFVRYAYAKWIKII 720 661 aekigsgpcgqyggplvceqhmrvlvivpgrcalipnrgrifvryayakwikkii 720 Db 721 LTYKVPQS 728 QY 721 ltykvpqs 728 Db 721 ltykvpqs 728 </p>
PS	<p>Query Match 100 %; Score 4126; DB 17; Length 728; Best Local Similarity 100 %; Pred. No. 9.5e-277; Indels 0; Gaps 0; Matches 728; Conservative 0; Mismatches 0;</p> <p>QY 1 MWVTKLPAULLQHVLHLLPLTAIPAYAEGQRKRNTIHEFKSAKTLIKIDPALKIK 60 1 mwvtkilpalilqlvhvihllplaiyaaegqrkrntihfksaktlidpalkik 60 QY 61 TKKVNADOCANCRTRNKGKLPFTCKAKFVKDARKOCLWFPPNSMSGVKEFGHEDLYE 120 61 tkkvnadqganrcntrnkgkpfckafvfarkqklwfpsmsggvkfkgfhefdlye 120 Db 121 NKDYIRNCITGKGSKYKGTVTSKSGKICOPWSSMIPHESFLPSYRGKQLOQENYCRNP 180 QY 121 nkdylircnclgkgrsykgtvtsksgkicopwssmiphensfipssyrgkqloqenycrnp 180 </p>

QY	181	ROEEGGPWFCSNPENVKEVCDIPOSESEWCNTGNSRSYRGMIDHESKGTCQRWHQTP	240
FT	Domain	/label= Kringle_3_domain	391..464
FT	rgeeggpwctfsnperryevdipqosevecmctngesyrqlmdheskgcqrwahqt	/label= Kringle_4_domain	294
FT	181 rgeeggpwctfsnperryevdipqosevecmctngesyrqlmdheskgcqrwahqt	/label= N-linked_glycosylation_site	294
FT	241 HHKFLPERYPKGDDNYCRNPDGSPRPWCYTLDDHTREWCAYTCAITCADCWMDTDVPL	/label= N-linked_glycosylation_site	402
FT	241 hnhkfiperypkgfdanycrtpdqgrprwcylabtrweycaitcaditcaitlndtavp	/label= N-linked_glycosylation_site	300
FT	301 ETECLOGEYRGVTNTIWNGIPQRWDQSYPHEDMTENFKCKDLRENYCRNPDGS	/label= N-linked_glycosylation_site	360
FT	301 etteciqgqgedgyrgvtntiwngipeqrwsqyphedamtptenkdkdrrenycrndgs	/label= N-linked_glycosylation_site	360
FT	361 ESPWCFTMDPNIRVGCSQIPNCMDMGRQDCYRGNENYMGMSQPRSGLICSMWKRNME	/note= "Position of opt. substitution, esp. Glu, Asp or Asn"	420
FT	361 espwcfcttdpnirvgcsqipncmdmshgqdcyrgnknymqnglnsqtsqrltcsmwkmne	/note= "Position of opt. substitution, esp. Tyr or Phe"	420
FT	421 DIHRHTWEPDASKLNEYCRNPPDDAHAHPCTGPAUTGPIRSCEDDTPTIVNL	/note= "Position of opt. substitution"	480
FT	421 dhrhhtwepdasklhenycrnpdddaahhpctgpautgpiirsceddtptivnl	/note= "Position of opt. substitution"	480
FT	481 DHVISCAKKTOLRVNGIPTPTNIGMWNSLRYNKHICCGSLIKESWLTAROCFPSRD	Misc-difference 673	540
FT	481 dhviscaktqlrvngiprttnigwmssrynkhicggslikeswltarocfpsrd	/note= "Position of opt. substitution"	540
FT	541 LRDYEAMLGILHDVGRDDECKKQVLNVLSQVYGPESDLVMLKLPAPVLDVFSTIDP	PR 13-JUL-1993; 92US-0087783.	600
FT	541 lkydewalgnihavhrgdekkcqvlkvlnksplavdftstidp	PR 18-MAY-1992; 92US-0084811.	600
FT	601 NYGCTPEKTSQSYKGTYGLINVQLLRVAHYIMGNEKCSQHKGKVLINESEICAG	PR 18-MAY-1992; 92US-0085971.	660
FT	601 nygtiptektsqsykgtyglinvqllrvahlyingnekcsqhqrgkvltineicag	PR 18-MAY-1992; 92US-0085971.	660
FT	661 AEKIGSOPCEGYGGPVLCEOHKMRMVLGVIVPGRGCAIPNRPGIVRVAYAKWHLKI	XX (GETH) GENENTECH INC.	720
FT	661 aekigsgpcggdyggpvlceqghkmrmvlgivpgrcainprgivrvayakwhlki	XX Godowski PJ, Lokker NR, Mark MR;	720
FT	721 ITYKVROS 728	XX DR WPI, 1996-392634/39.	721
FT	721 itykvpas 728	XX PT New hepatocyte growth factor variants - are resistant to in vivo proteolytic cleavage into a 2-chain form, useful as HGF antagonists	721
FT	721 itykvpas 728	XX PS Disclosure; Column 51-56; 39pp; English.	721
RESULT	3		
AAW00340	AAW00340 standard; protein: 728 AA.		
ID	XX		
AAW00340;	XX		
09-DEC-1996	(first entry)		
XX	Wild type hepatocyte growth factor.		
DE	Human; hepatocyte growth factor; HGF; human; serum; proteolytic cleavage; pro-hormone; beta subunit; alpha subunit; kringle domain; prothrombin; plasminogen; catalytic domain; serine protease; HGF variant; HGF receptor; malignancy; chronic HGF receptor activation.		
KW	OS Homo sapiens.		
XX	Key Location/qualifiers		
FT	Cleavage-site /label= Proteolytic cleavage_site		
FT	/note= "generates alpha and beta subunits"		
FT	Disulfide-bond 1..54		
FT	Peptide 1..31		
FT	/note= "Hydrophobic signal peptide"		
FT	Domain 128..206		
FT	/label= Kringle_1_domain		
FT	Domain 211..288		
FT	/label= Kringle_2_domain		
FT	Domain 303..383		
Query Match	100.0%	Score 4126; DB 17; Length 728;	
Best Local Similarity	100.0%	Pred. No. 9 5e-277;	
Matches	728;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MAVTKLQLPALLQHVLLPLPIALPYAEGRKRWRMHEFKKSATLKLIDPALIK	CC	50
DB	1 mawtklqlpallqhvlhllplpialpyaeqrkrwrmkksatlkklidpalik	CC	60

QY	61	TKKVNTADOCANRCTRNKGKGLPTCKAFVFKARKOCLWPFNSMSGVKREFGFHFDLYE	PA
			XX
Db	61	tkkvntadocanrcnctrnkgkglptckafvfkarkoclwfpfnsmsgvkrefgfhdlye	PI
			PI
QY	121	NKDYIRNCITIGKGRSYKGVTSITSGIKQPMWSSMIPHHSFLPSSYRKDLOQENCRNP	DR
			N-PSDB; AAV53626.
Db	121	nkdyirncitigkgrsykgtvsitsgikqpmwssmiphhflpsysyrdloqencrnp	DR
			XX
QY	181	RGEDEGGWCETSNPERRYEVCDIPOCSEECMTNGESRGLMDHTESKICQRMHDOTP	PT
			Preparation of recombinant hepatocyte growth factor polypeptide - by
Db	181	rgeeggpwcftsnperryevcdiqpcseecmtngesryglmdhteskicqwdhqt	PT
			culturing mammalian cells transformed with vector containing human
QY	241	HRHKFLPERYPDKGDDNNCRNPDQCPRWYCYTLDPTHECAIKTCADNTMDTDVPL	PT
			leukocyte-derived HGF gene
Db	241	hrhkflperypdkfdanycrnpdgq-pwcytldphtrwcaiktcaadntmdtdvpl	PT
			XX
QY	301	ETTECIOCGCGEGYGTNTWINGTPCQRDSDQYRHEDMTPENFKCKDIRENYCRNPDS	PS
			Claim 1; Fig 2a-c; 30pp; English.
Db	301	etteciocgcgegygtntwinqpcqrwsqphedamtpefkckdirenycrnpgs	XX
			This is the amino acid sequence for human leukocyte-derived
QY	361	ESPCFRTTPNIRYGCQIIPNCDMSHGQCYRNGKWMGNLSQTRSGLTCSWMDKNE	CC
			hepatocyte growth factor (HGF), deduced from a cDNA clone
Db	361	espwfcttcapnirygcsqipnacdmshgqcyrgngknymqnlsgtsqrltcsmdkne	CC
			(see AAV53626) obtained from a leukocyte cDNA library. Another
QY	421	DLRRHFEPDASKLNEYCRNPDQDAHGPWCYTGNPLIPWDYCPCISRCEDDTPTVNL	CC
			leukocyte-derived HGF, HLC2 (see AAV5923), was identified that
Db	421	dhrhfepdasklnenycrnpddahgpwcytgnplipwdycpcisrceddtptvnl	CC
			differs from HLC3 by having amino acid residues 162-166 deleted.
QY	481	DHPVISCAKTOLRUVNGTPTRANGTGWMWSLRTRNHKGGSIIKESWMLTAQCFSRD	CC
			A claimed method of producing HGF comprises: transforming
Db	481	dhpviscaktkqlrvngtptrangtgwmwslyrnkhicggslikeswtarqcfbsrd	CC
			mammalian cells (preferably CHO cells) with a recombinant
QY	541	LKYEWAWLGHDYGRGUBBCKOYLNVLSQVWPEGSQDILMLARPWLDPVSTIDP	CC
			gene coding for human leukocyte-derived HGF, and the
Db	541	lkyewawlgihdvingrqgdekkavlnqvlygpegsdlvmlklarpavaldffvstdlp	CC
			dihydrofolate reductase gene; (b) culturing the transformed cells
QY	601	NYCCTIPEKTSCSVYWGWTGLINQDGULLRVALYIMNNEKEQSQHHRGKVTUNESELAG	CC
			in the presence of successively elevated concentrations of
Db	601	nyctipektscsvywgwtglinydgullrvalyimnnekqsqhhrqktineseicag	CC
			methotrexate; and (c) recovering the HGF polypeptide from the
QY	661	AEKIGSGPCEGDDYGGPLVCEOHKMRMVGIVVGRGCAIPNRGIFPRVAYAKWIKI	CC
			culture supernatant. HGF polypeptides may be used as hepatocyte
Db	661	aekigsgpcegddygplvceohkmrmvgivvgrgcaipnrqifprvayakwikk	CC
			cultivation reagents, liver regeneration promoters, in basic
QY	721	LTVKVPQS 728	CC
			research on liver function, research on the action of various
Db	721	ltvkvpqs 728	CC
			hormones and drugs on hepatocytes, research on the carcinogenesis
			mechanism of hepatoma, clinical diagnostic reagents using an
			antibody against the polypeptide and therapeutic drugs for liver
			disease.
SQ	Sequence	728 AA;	XX
	Query Match	100.0%	XX
	Best local Similarity	100.0%	XX
	Matches	728;	XX
	Conservative	0;	XX
	Mismatches	0;	XX
	Indels	0;	XX
	Gaps	0;	XX
QY	1	MWYTKLIPALIQHVLILLIPILIAPIAYAEGOKRKRRTIHEFKSKATLKLIDALKIK	XX
			XX
Db	1	mwytklipalilqhvllillipiliaapiayeqkrkrrihefkskttlkilidalkik	XX
			XX
QY	61	TKKVNTADOCANRCTRNKGKGLPTCKAFVFKARKOCLWPFNSMSGVKKEFGHERDLYE	XX
			XX
Db	61	tkkvntadocanrcnctrnkgkglptckafvfkarkoclwfpfnsmsgvkkefghefdlye	XX
			XX
QY	121	NKDYIRNCITIGKGRSYKGVTSITSGIKQPMWSSMIPHHSFLPSSYRKDLOQENCRNP	XX
			XX
Db	121	nkdyirncitigkgrsykgtvsitsgikqpmwssmiphhflpsysyrdloqencrnp	XX
			XX
QY	181	RGEDEGGWCETSNPERRYEVCDIPOCSEECMTNGESRGLMDHTESKICQRMHDOTP	XX
			XX
Db	181	rgeeggpwcftsnperryevcdiqpcseecmtngesryglmdhteskicqwdhqt	XX
			XX
QY	241	HRHKFLPERYPDKGDDNNCRNPDQCPRWYCYTLDPTHECAIKTCADNTMDTDVPL	XX
			XX
Db	241	hrhkflperypdkfdanycrnpdgq-pwcytldphtrwcaiktcaadntmdtdvpl	XX
			XX
QY	301	ETTECIOCGCGEGYGTNTWINGTPCQRDSDQYRHEDMTPENFKCKDIRENYCRNPDS	XX
			XX
Db	301	etteciocgcgegygtntwinqpcqrwsqphedamtpefkckdirenycrnpgs	XX
			XX
QY	361	ESPCFRTTPNIRYGCQIIPNCDMSHGQCYRNGKWMGNLSQTRSGLTCSWMDKNE	XX
			XX
Db	361	espwfcttcapnirygcsqipnacdmshgqcyrgngknymqnlsgtsqrltcsmdkne	XX
			XX
QY	421	DLRRHFEPDASKLNEYCRNPDQDAHGPWCYTGNPLIPWDYCPCISRCEDDTPTVNL	XX
			XX
Db	421	dhrhfepdasklnenycrnpddahgpwcytgnplipwdycpcisrceddtptvnl	XX
			XX

OY 481 DHPVISCAKTKOLRVNGIPTNTNIGMNSLRYRKHICGGSLIKESWLTARQCPQRD 540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 dhpviscaktkqlrvngiptrnigmslrnyrkhhicggslikeswltarqcpqr 540
 OY 541 LKDEAWLGHIDVHGRGDECKQVNLNVSQLVNGPEGSIDLMLKARPAVLDDFVSTIDLP 600
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 541 lkdeawlgindvhg-rg-deckqkvlnsqlyygepgsdlvmlklaapaviddfvsidlp 600
 OY 601 NYGCTIPERKTSCSVYWGTYGLINQGLRVAHYLYMNEKCSOHRGKVNLNESEICAG 660
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 601 nyctipektscsvywgtyglinydglrrvahlyingneksqhnrgkvtneseicag 660
 OY 661 AEKIGSGPCEGDYGPPLUCEQHMMRMVLGVYVPGRCAPNRPGIFRVAYAKWIHKII 720
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 661 aekigsgpcegdyygpvlceqhkmrmvlgvivpgrgcaipnrgifrvayakwihi 720
 OY 721 LTVKVPQS 728
 |||||
 721 ltvkvpqs 728

RESULT 5
 AAWS656 standard; protein: 728 AA.
 ID AAWS656
 AC AAW58696;
 DT 08-SEP-1998 (first entry)
 DE Human hepatocyte growth factor.
 KW Human; hepatocyte growth factor; HGF; high blood sugar.
 OS Homo sapiens.
 PN JP10167981-A.
 XX 23-JUN-1998.
 PD XX
 PF 09-DEC-1996; 96JP-0328357.
 PR XX
 PR 09-DEC-1996; 96JP-0328357.
 PA XX
 PA (MITU) MITSUBISHI CHEM CORP.
 XX WPI; 1998-408607/35.

New preventive and/or treating agent - comprises hepatocyte growth factor, used for diseases caused by high blood sugar

XX PS Claim 5; Page 4-6; 6pp; Japanese.

CC The present sequence represents human hepatocyte growth factor (HGF). A preventive and/or treating agent for the diseases caused by high blood sugar has been developed. The agent comprises HGF as an active component. The preventive and/or treating agent causes no excessively low blood sugar.

SQ Sequence 728 AA;

Query Match 100.0%; Score 4126; DB 19; Length 728;
 Best Local Similarity 100.0%; Pred. No. 9_5e-277; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAWTKLILLQHVLHLILPIATYAEGRKRRNTHIEFKSAKITLIRKIDPAKIK 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 mawtklillqhvlhlilpiatyaegrkrntheffksakitlirkidpalkik 60
 61 TKEVNTADQANRTRKNGLPCTKARVFDKARKQCLWPFENMSMSSVKERGEFLYE 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 tkevntadqancctrknglpctkarkqclwfpfsmssvkkegheroflye 120

RESULT 6
 AAWS2998 standard; protein: 728 AA.
 ID AAWS2998
 AC AAW42998;
 DT 23-JUL-1998 (first entry)
 DE Recombinant human hepatocyte growth factor (HGF).
 KW hepatocyte growth factor; HGF; W/O/W emulsion; blood half life; therapeutic; drug; hepatic tissue; hepatic disease; acute hepatitis; chronic hepatitis.
 KW Homo sapiens.
 OS Homo sapiens.
 PN JP10007387-A.
 XX 13-JAN-1998.
 PD 24-JUN-1996; 96JP-0163063.
 PR XX
 PA (AZUMA) AZUMA H.
 PA (MITU) MITSUBISHI CHEM CORP.
 PA (MIYA) MIYAZAKI KEN.
 PA (TSUB) TSUBOUCHI H.

QY 121 NKDYIRNCIGKRSYKCTVSIKSGIKCOPWSSMIEHEHSLPSSYRGKDQENYCRNP 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 nkyirncigkrsykytvsitskgikcopicwsmihehsflpsyrgkdqenynrp 180
 OY 181 RGEEGGPWCFTSNPEVRVECDTIPQCSCEVCWMTONGESYRGLMDHTESGKICQRWDHQTP 240
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 rgeeggpwcfstspvryevcdlpcsevecmtcngesyrqmdhtesgkicqrwdhqtp 240
 OY 241 HRKFLPERPYDPKGFDNYCRAPDGOPRWPCYTLDPHRWECAIKCADCNTMDVPL 300
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 hrkflperpydpkgfdanycrapdgqprpwcytlphtrweycaiktcadntmdvpl 300
 OY 301 ETTECIOQGEGRGRTWTIWNQPCQRWDQSYPHERDMTPENFKCDLRENWCRNPDGS 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 ettecioqgegrgrytvtningipcqwdqsyphenmdtpenfkcdlrenycrpds 360
 OY 361 ESPWCFTTDPPNIRVGYSQQPNQDMSHQDQCYRGNKNYMGNIQSQTSGLTCMWDKME 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 espwcfttdppnirvgysqqpnqdmshqdcyrgnknymgnlsqtsgltcosmwdkme 420
 QY 421 DLURHIFWEPDASKLNENYCNPDDAHPGWCTGNPLIPWYCPSTSCEGJPTPTVNL 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 dlurhifwepdasklnenycnpddahpgwcytgnplicpdcrgatptvnl 480
 OY 481 DHVISCAKTKOLRVNGIPTNTNIGMNSLRYRKHICGGSLIKESWLTARQCPQRD 540
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 dhviscaktkqlrvngiptrnigmslrnyrkhhicggslikeswltarqcpqr 540
 OY 541 LKDEAWLGHIDVHGRGDECKQVNLNVSQLVNGPEGSIDLMLKARPAVLDDFVSTIDLP 600
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 541 lkdeawlgindvhg-rg-deckqkvlnsqlyygepgsdlvmlklaapaviddfvsidlp 600
 QY 601 NYGCTIPERKTSCSVYWGTYGLINQGLRVAHYLYMNEKCSOHRGKVNLNESEICAG 660
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 601 nyctipektscsvywgtyglinydglrrvahlyingneksqhnrgkvtneseicag 660
 OY 661 AEKIGSGPCEGDYGPPLUCEQHMMRMVLGVYVPGRCAPNRPGIFRVAYAKWIHKII 720.
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 661 aekigsgpcegdyygpvlceqhkmrmvlgvivpgrgcaipnrgifrvayayakwihi 720
 OY 721 LTVKVPQS 728
 |||||
 Db 721 ltvkvpqs 728

	SQ	Sequence	728 AA.
Db	301	ettec1cqgqegyrgtvnt1ngipocqrwqsqyphedmtpenfkcdlrenycrndgs	360
QY	361	ESPWCFITDPNIRVYGCQSQIPNCDSHQDCYRGKNGKNMQLSQTSGLTCSMMWDKNAME	420
Db	361	espcwcfittdpnirvycsqipncdmshqdcyrgkngknmqlsqtsgltcsmmwdkname	420
QY	421	DLHRHIFWEDASKLNENYCNRNPDDAHAHGWCYTGPNLIPMDYCISRCEDDTPTIVNL	480
Db	421	dhrifwepdasklnenycnrpddahgwcyclplipwcyisrceddtptivnl	480
QY	481	DHPV1SCAKTKQLRVLVNGIPTRTNIGMWMSRYRNKHICGSLLIESWVJAROCFPSRD	540
Db	481	dhpviscaktqlrlvngiptrtnigmwmsryrnkhicgsllieswvitarqcfsrd	540
QY	541	LKDYEAWLGHDVRGDEKCKQKVNLNSOLVYGPQSDLVMLKLRPAVIDEVSTIDLP	600
QY	541	lkdyawlgihavhrgedekckqvlnvsqivygpegsdlvmlkarpaividfvstidlp	600
QY	601	NYGCTIPEKTSVYVGWGYGLINDGLRLVHLVHLYMGNEKCSQHHRGKVTLINESETCAG	660
QY	601	nygti-pektscsvyvgwyglindglrlvhlymgnekcsqhsrqkvtlineicag	660
QY	661	AEKIGSSPCEGDYGPVLCEOKHMRAVLGV1VPGRCALIPRPGFVRVAYAKWHKII	720
Db	661	aekigspscggdgypvlceokhmrvmlgv1vpgcaiprpgfvrveyakwhkii	720
QY	721	LTYKQPOS 728	
Db	721	ltykvpqs 728	
RESULT	8		
ID	AAR39521	standard; Protein; 728 AA.	
XX			
AC	AAR39521;		
XX			
DT	20-SEP-1993	(first entry)	
DE		Hepatocyte growth factor.	
KW		HGF; side effect; cancer; tumour; chemotherapy; radiotherapy; carcinostatic.	
OS		Synthetic.	
XX			
WO9308821-A.			
	13-MAY-1993.		
XX			
PF	05-NOV-1992;	92WO-JP01433.	
XX			
PR	07-NOV-1991;	91JP-0321412.	
XX			
PA	(NAKA,)	NAKAMURA T.	
XX			
PI	Nakamura T;		
DR			
WPI:	1993-167384/20.		
DR	N-PSDB; ARA46040.		
XX			
PT		Side effect inhibitor for cancer therapy - containing hepatocyte growth factor and inhibiting side effects resulting from treatment by chemotherapy, radiotherapy	
PT		Since HGF alleviates damage to normal cells and tissues, it can inhibit side effects in treating cancers by chemotherapy, radiotherapy, etc. With it, it is possible to conduct more intense cancer therapy and to improve the carcinostatic effects. It is extremely useful in the field of clinical medicine.	
PS			
CC			
XX			
RESULT	9		
ID	ARR25676	standard; protein; 728 AA.	
XX			
AC	AAR25676;		
XX			
DT	20-JAN-1993	(first entry)	
XX			
DE		Recombinant human hepatocyte growth factor.	
XX			
KW		HGF; enhance growth; preparing transgenic animals; hepatic disease; clinical diagnostic reagent; drug.	
XX			

Db	61 tkkvntadqcanctrnkgpltkarfvdkarkqcilwfpfnsmsgvkerghfelye	120	XX	
Qy	121 NKDVRNCITIGKGRSYKGCTVSTIKSGIKCOPRSMITHESNLSSYRGKDQENYCRNP	180	DR N-PSDB; AAQ20049.	
Db	121 nkyiricqigqrsyitksgikcpwsmiphesflpsyrkgdqlqenycrnp	180	PT Agent contg. hepatocyte growth factor and carrier - used for treating renal diseases and promoting nephrocyte growth and as diagnostic for renal diseases	
Qy	181 RGEFGPWCFTSNPEVREVCDFPQSEVECMTCNGESYRGLMDHTSGKLCQRWDHOTP	240	PT XX	
Db	181 rgeggpwftsnpevrevcdipqcssevcmtngesyrqldmhtesgkicqrwdhqt p	240	PS XX	
Qy	241 HRHKFLPERYPKGFDNYCRPDGQRPWCFLDPIRWECAIKCADCNTMDTIVPL	300	Human HGF comprises an alpha-chain of 440 amino acids and a beta-chain of 234 amino acids. There are 4 kringle domains in the alpha-chain, similar to that of plasmin; the beta-chain has about 37 per cent homology with the beta-chain of plasmin having serine protease activity. Homology of the amino acid sequence of rat HGF and human HGF is 91.6 per cent in the alpha chain and 88.9 per cent in the beta-chain. HGF has been found to be an agent for nephrocyte growth and is useful as a treatment for renal failure.	
Db	301 ETECIOQGEGYRTNTIWNQPCQRMDSQYRHEHDMPENFKCDLRENCRNPDGS	360	CC CC CC CC CC CC XX	
Db	301 ettecqgqgeyrtntiwnqpcqrwdswsyphendmtfkcdlreycrpdgs	360	Sequence 728 AA: Query Match 99.8%; Score 4118; DB 13; Length 728; Best Local Similarity 99.9%; Pred. No. 3.4e-27; Indels 0; Gaps 0; Matches 727; Conservative 0; Mismatches 1; Gaps 0;	
Db	421 dhrhifwepdasklnenyrcnpddahgpcwytgnplipwypcrscegttptivnl	480	Qy 1 MWYTKLLPALLPHOLVHLUILLPLAIPYAEGORRKRNTHFRKSAKTLIKDALKIK 60 Db 1 mwytkilpalllhglvhlillplaiplaipyaeqgrkrntihfsakttlidpalkik 60	
Qy	481 DHPVISCAKTKLQRVNGTPTRNIGMVGMSLVRNKHCGSLIKESWLARQCFSRD	540	Qy 61 TKKVNTADQCANCTRNGKLGPFCKAFVFDKARKQCLMPPFNSMSCYKKFGEHFDLYE 120 Db 61 tkkvntadqcanctrnkgpltkarfvdkarkqcilwfpfnsmsgvkerghfelye 120	
Db	481 dhpviscaktklqrvgvqiptnqmglnstqrlsqtsgltcsmwdkme	540	Qy 121 NKDVRNCITIGKGRSYKGCTVSTIKSGIKCOPRSMITHESNLSSYRGKDQENYCRNP	180
Qy	541 LKDYEAWLGIDHYGRGDECKQKVLNNSQLVVGPGESDLVLMKLARPAVLDDFVSTIDLP	600	Db 121 nkyiricqigqrsyitksgikcpwsmiphesflpsyrkgdqlqenycrnp	180
Db	541 lkyewalighdrgrdeckqkvlnvsqlyvgpegsdlvilmklarpaviddfvtidlp	600	Qy 181 RGEFGPWCFTSNPEVREVCDFPQSEVECMTCNGESYRGLMDHTSGKLCQRWDHOTP	240
Qy	601 NYGCTIPKTSVYGMGTYGLINYDGLRLRVHLYINGNEKEQSQHNGKVTLNESECAG	660	Db 181 rgeggpwftsnpevrevcdipqcssevcmtngesyrqldmhtesgkicqrwdhqt p	240
Db	601 nygtipektscsvywgtyglinydglrlrvahlyingnekcsqhqrgkvtneseicag	660	Qy 241 HRHKFLPERYPKGFDNYCRPDGQRPWCFLDPIRWECAIKCADCNTMDTIVPL	300
Qy	661 AEKIGSPCEGGYGLPVCQHKRMVLGVIVPGRGCAIPNRPGIFRVAYYAKWIHKII	720	Db 241 hrhkifwepdasklnenyrcnpddahgpcwytgnplipwypcrscegttptivnl	300
Db	661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720	Qy 301 ETECIOQGEGYRTNTIWNQPCQRMDSQYRHEHDMPENFKCDLRENCRNPDGS	360
Qy	721 LTYKVPQS 728	728	Db 301 ettecqgqgeyrtntiwnqpcqrwdswsyphendmtfkcdlreycrpdgs	360
Db	721 Ltykvpqs 728	728	Qy 361 ESPWCFTDPNIRVGCSQIPNCDMSHQDCYRGNKNMGNIQSRTGLCSMWDKME	420
	JULY 11		Db 361 espwcftrdpnirvgcsqlpncdmshqdcyrgngknymnlsqtsgltcsmwdkme	420
ARR2005			Qy 421 DHRHIFWEPDASKLNENYCRNDDAHGPWCYTGNPLIPWYDPCPISRCEGTTPTIVNL	480
ID	AAR2005 standard: Protein: 728 AA.		Db 421 dhrhifwepdasklnenyrcnpddahgpcwytgnplipwypcrscegttptivnl	480
XX			Qy 481 DHPVISCAKTKLQRVNGTPTRNIGMVGMSLVRNKHCGSLIKESWLARQCFSRD	540
AC	AAR2005;		Db 481 dhpviscaktklqrvgvqiptnqmglnstqrlsqtsgltcsmwdkme	540
XX	24-MAR-1992 (first entry)		Qy 541 LKDYEAWLGIDHYGRGDECKQKVLNNSQLVVGPGESDLVLMKLARPAVLDDFVSTIDLP	600
DT	Human hepatocyte growth factor.		Db 541 lkyewalighdrgrdeckqkvlnvsqlyvgpegsdlvilmklarpaviddfvtidlp	600
XX	HGF: kidney regeneration; nephritis.		Qy 601 NYGCTIPKTSVYGMGTYGLINYDGLRLRVHLYINGNEKEQSQHNGKVTLNESECAG	660
KW	Homo sapiens.		Db 601 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
XX			Qy 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
OS			Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
XX			Qy 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
EP462549-A.			Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
XX			Qy 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
PD	27-DEC-1991.		Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
XX	18-JUN-1991; 91EP-0109923.		Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
PR	19-JUN-1990; 90JP-0158841.		Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
XX	(TOYM) TOYO BOSERI KK.		Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
PA			Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720
XX	Nakamuro T;		Db 661 aekigspscggdygpvcqhkrmvlqvivpgrcainpnrgifvrvayyakwihi 720	720

Qy 721 LTYKVQPS 728
 Db |||||||
 Db 721 ltykvqps 728

RESULT 12
 AAW88529
 ID AAW88529 standard; protein; 728 AA.
 XX
 AC AAW88529;
 XX
 DT 02-MAR-1999 (first entry)
 DE Human hepatocyte growth factor (HGF) variant 1.
 KW Human; HGF; hepatocyte growth factor; variant; HGF receptor; medicine; heparan sulphate proteoglycan; cancer.
 OS Homo sapiens.
 Synthetic.

Key Location/qualifiers

FT Misc-difference 73
 FT /label= R33E
 FT /note= "wild-type Arg is replaced with Glu"
 FT Misc-difference 76
 FT /label= R76E
 FT /note= "wild-type Arg is replaced with Glu"
 PN W09851798-A1.
 XX PD 19-NOV-1998.
 XX PP 07-MAY-1998; 98WO-GB01318.
 XX PR 10-MAY-1997; 97GB-0009453.
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX PT Birchmeier W, Gherardi E, Hartmann G;
 DR XX
 PT Hepatocyte growth factor variants - binding to hepatocyte growth factor receptor, useful in medicine e.g. for cancer therapy
 XX PS Claim 6; Page ; 75pp; English.

The present sequence represents a human hepatocyte growth factor (HGF) variant. The HGF variants are substantially unable to bind heparan sulphate proteoglycan. The HGF variants are useful in medicine e.g. variants having the same effects on target cells as wt-HGF can be administered to patients requiring HGF, while antagonistic variants can be administered to patients requiring HGF variants. They are especially useful for treating cancer. Some of the variants have a longer circulatory half-life in vivo and a greater mitogenic activity than wt-HGF in rats. They are therefore useful therapeutically as wt-HGF, but may have superior effects in vivo e.g. giving greater tissue penetration and ability to reach cell or tissue compartments.

Note: This sequence is not provided in the specification; it has been created by modifying the wild-type HGF sequence.

Sequence 728 AA:

Db 1 mwvttkl1palllqlhvllhlplialpyaqeqqrkrntihfksaktlikdpalkik 60
 Qy 61 TKVNRAQCANRCTRNKGKLFPTCKRAFKVERKARKOCLWPFPPNSMSSCYKKERHEFDYE 120
 Db 61 tkkvntadgconnectenkqkpfctafavfkarkkclwlfpfnfnsnsgykkefghedfyle 120
 RESULT 13
 AAR10656
 ID AAR10656 standard; Protein; 727 AA.
 XX
 AC AAR10656;
 XX
 DT 16-APR-1991 (first entry)
 DE Hepatic parenchymal cell growth factor.
 KW Hepatic parenchymal cell growth factor; cirrhosis.
 OS Homo sapiens.
 XX
 Key Location/Qualifiers
 FH Peptide 30..727
 FT Peptide /label= hGIF active fragment
 FT Peptide 32..727
 FT /label= hGIF active fragment
 PN EP412557-A.

Query Match 99.8%; Score 4116; DB 20; Length 728;
 Best Local Similarity 99.7%; Pred. No. 4; 7e-276;
 Matches 726; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MWVTKLPLALLQHVLLHLPLIPTYASGORKRNTTHEFKSAKTLIKIDPALKIK 60
 |||||||

Note: This sequence is not provided in the specification; it has been created by modifying the wild-type HGF sequence.

CC	KW
CC	Hepatocyte growth factor; liver; hepatoma.
XX	XX
SQ	OS
	Homo sapiens.
	XX
	PN
	XX
	PD
	XX
	PX
	07-JUN-1991; 91EP-0109369.
	XX
	PR
	11-JUN-1990; 90JP-0152474.
	XX
	PA
	(TOYM) TOYO BOSEKI KK.
	XX
	PX
	Nakamura T, Hagiya M, Seki T, Shimonishi M, Shimizu S;
	PI
	Iharai, Sakaguchi M, Asami O;
	XX
	DR
	WPI; 1991-370578/51.
	DR
	N-PDB; AAQ15176.
	XX
	PT
	Recombinant human leukocyte-derived hepatocyte growth factor -
	PT
	with DNA encoding it, recombinant expression vectors and
	PT
	transformant cells expressing it.
	XX
	PS
	Claim 2; Fig 2; 33pp; English.
	XX
	The sequence was deduced from a portion of HLC2, one of two clones (for HLC3 see ARI15624) isolated from a cDNA library prep'd. from mRNA extracted from human leukocytes. HLC2 has almost the same sequence as HLC3 except for five residues, 162-166, which do not appear in HLC3. The DNA sequence can be expressed and the resulting protein, recombinant HGF, used in hepatocyte cultivation, liver regeneration, hepatocyte research, esp. the mechanism of hepatoma, and to prepare anti-HGF antibodies for diagnosis and therapy.
	CC
	XX
	SQ
	Sequence 728 AA;

Query Match	99.7%	Score 4113; DB 20; Length 728;
Best Local Similarity	99.6%	Pred. No. 7.5e-276; Mismatches 1; Indels 0; Gaps 0;
Matches	725;	Conservative 2;
Sequence	728 AA;	
QY	1 MWYVKKLPLALLQVLLHILLPATAIPVAGQRKRNTTHEFKKSAKTLIKDPAIK 60	
Db	1 mwvtkkllpallqlvhvllplaiplaipyagqrkrntihefkkksaktlikdpaik 60	
QY	61 TKKNTADOCANTRNKKLPFTCKAFVFDKAROCLWFPPNSMSSGUKKEFHEFDLYE 120	
Db	61 tkkvntadocanctrnkklpftckafvfdkarkqcwfppnsmssgukkefhefdlye 120	
QY	121 NDKVIRNCITGKGSYKGWSITKSGIKQWPSSMIPHEFESYRGKDLQENYCNP 180	
Db	121 ndkvircigkgsykgwsitksgikqwpssmiphefsipsyrgkdlqenycnp 180	
QY	181 RGEDEGGPMCFTSNEPVREVCDFQOCSEVCMTCNGESYRGLMDHTESGKICORWDHOP 240	
Db	181 rgeeggpmcfstnspevrevcdlpcqsevcemtcngesyrglmdhtesgkicrdqngtp 240	
QY	301 ETTECIOQGEGGRGTVTNTIWINGIPCPQRCDSQPHEDMTPENFKCOLRENCRNPGS 360	
Db	301 etteciqgggegyrgtvtntiwinjpcqcpwdsqphedantpenfkclrenycrnpgs 360	
QY	361 ESPCQFTTDPNIRGYCSPQNCMDMSHGDCYNGKNGMNSQTREGTCSMDKME 420	
Db	361 espwfttppknirgycspqncmdmshgdcyngkngmnsqtregtcsmdkme 420	
QY	421 DLHRHFWRPDASKLNEYCNRPDDAHPQWCYTGNPLPFWYCAIKTCADNTMDTDVPL 300	
Db	421 dhrhifwepdasklnenyccrnppddangpwyctgnplipwdcpiscegdtptivnl 480	
QY	421 DHPYFISCAKTKQKRVNGIPTRNIGWMWLSRFRNKHCGGSLIKESWNLARQCFPSRD 540	
Db	421 dhpviscaktkqirkvngiptrtnigwmwlsrfrnkhhcgsslikewnlarqcfpsrd 540	
QY	541 LKDYEAWLGHIDYGRGDBCKQDVLNSOLVYGRPEGSIDLVLKCARPAVLDDSTIDLP 600	
Db	541 lkdyjawlgihdvhgrrgdekkqylvlnsqvlyyppesdvlvmlkarpvlddfstidlp 600	
QY	601 NYGGTPEKTMSCSYWGWTGLINYGDLIRVAHYIYMGNEKCQSOHRGKVTLNESEIAG 660	
Db	601 nyggttpektscsywgwtglinydglirvanhyimgnekcqsohrgvtkvtneseicag 660	
QY	661 AEKGSGSGCEGDYGGPLCQEOKHMRMVGIVPGRGCAIPNRGCFIVRVAAYKKWHKT 720	
Db	661 aeklgsgsgcegdyyggplveeqhkmrmvgivvprgcaipnrpgifrvayakkwhkt 720	
QY	721 LTVKVPQS 728	
Db	721 ltvkvpqs 728	
RESULT 1;		
ID ARI15623	AARI15623 standard; Protein: 728 AA.	
XX		
XX		
XX		
DT 18-MAR-1992 (first entry)		
XX		
DE Human leukocyte-derived HGF encoded by clone HLC2.		
XX		

OY 481 DHPVIECAKTKQLRVRNGTPTRTNCWMSLRYRNHICGSSLIKPSWLTAQCPSPRD 540
Db 481 dhpviscaktkqlrvngiptrtncwmslryrnhicggsslikeswtarqcipsrd 540
OY 541 LKDYEAWLGIHDVHGSGDEKKQVNLNVSQLYGPGCSDLVIMKLARPAVIDDFVSTIDLP 600
Db 541 lkdyeawlgihdvhgsgdekkqvlvnsqlygpgcndlmlarpaviddfvstidlp 600
OY 601 NYGCCTPEKTSCSVKGWGYGLINTGCLRLVAHLYIMNEKCSQHHRGKVILNESETCAG 660
Db 601 nyctipektscsvywgqjinqglrvahlyingnecksburghgvilnesicag 660
OY 661 AEKIGSGPCEGDYGGPLVCEOHKMRAYLGVTVPGRCALPNRPGEFURVAVYAKWHTKT 720
Db 661 aekigsgpcegdyyggplvceohkmrnylvippgicainpgrifurvayyakwhtki 720
OY 721 LTYKVROS 728
721 ltykvros 728
721 ltykvros 728

Search completed: June 18, 2002, 17:46:59
Job time: 240 sec

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Om protein - protein search, using sw model

Run on:

June 18, 2002, 17:45:19 ; Search time 24.39 Seconds

(without alignments)

2868.103 Million cell updates/sec

Title: Perfect score:
Sequence: 1 MRVTKLLPALLQLQHVLHL... VAYYAKWIKHKLILTYKVPOQ 728

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Scored:

283138 seqs, 9608934 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 71;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	1	ALIGNMENTS
JH0579	hepatocyte growth factor precursor [validated] - human	coagulation factor
	N;Alternate names: heparoietin A; scatter factor	plasmin precursor
	C;Species: Homo sapiens (man)	coagulation factor
	C;Date: 17-Aug-1992 #sequence-revision 17-Aug-1992 #text_change 08-Dec-2000	plasma hyaluronan-
	C;Accession: JH0579; JU0333; A41140; B36677; A33512; A39006; PH0114; A37796;	plasminogen acti
	R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.	u-Plasminogen acti
	Gene 102, 213-219, 1991	t-Plasminogen acti
	A;Title: Organization of the human hepatocyte growth factor-encoding gene.	interpeptidase (E
	A;Reference number: JH0579; MUID:91340155	t-plasminogen acti
	A;Accession: JH0579	t-plasminogen acti
	A;Molecule type: DNA	tryptase (EC 3.4.2
	A;Residues: 1-728 <SEK>	
	A;Cross-references: DDBJ:D90318	
	A;Note: the authors translated the codon GAA for residue 662 as Gly	
	R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.	
	A;Description: Organization of the human hepatocyte growth factor-encoding gene.	
	A;Reference number: JH0579	
	A;Accession: JH0579	
	A;Molecule type: mRNA	
	A;Residues: 1-728 <SE2>	
	R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991	
	A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth hepatocyte growth	
	A;Reference number: A41140; MUID:91334393	
	A;Accession: A41140	
	A;Molecule type: mRNA	
	A;Residues: 1-728 <WE1>	
	A;Cross-references: GB:M73239; NID:9337935; PIDN:AAA64239_1; PID:9337936	
	R;Seki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya	
	A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor	
	A;Reference number: A36677; MUID:91025062	
	A;Accession: B36677	
	A;Molecule type: mRNA	
	A;Residues: 1-728 <SE3>	
	A;Cross-references: GB:M60718; NID:9184031; PIDN:AAA52648_1; PID:9184032	
	A;Accession: A36677	
	A;Molecule type: mRNA	
	A;Residues: 1-161,167-728 <SE4>	
	A;Cross-references: EMBL:X16323	
	A;Experimental source: leukocyte	
	R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nak	
	Biochem. Biophys. Res. Commun. 163, 967-973, 1989	
	A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth	
	A;Reference number: A33512; MUID:89392017	
	A;Accession: A33512	
	A;Status: not compared with conceptual translation	
	A;Molecule type: mRNA	
	A;Residues: 1-728 <MIY>	

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1	4126	100.0	728	1	JH0579		hepatocyte growth factor precursor [validated] - human
2	3804	92.2	728	1	A60185		N;Alternate names: heparoietin A; scatter factor
3	3802	92.1	728	1	A35644		C;Species: Homo sapiens (man)
4	2806	68.0	710	1	I51283		C;Date: 17-Aug-1992 #sequence-revision 17-Aug-1992 #text_change 08-Dec-2000
5	1821.5	44.1	411	2	I51285		R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
6	1652	40.0	711	1	A47136		Gene 102, 213-219, 1991
7	1615	39.1	716	1	JC0361		A;Title: Organization of the human hepatocyte growth factor-encoding gene.
8	1608	39.0	716	1	A0332		A;Reference number: JH0579; MUID:91340155
9	1446.5	35.1	790	1	PLBO		A;Accession: JH0579
10	1408.5	34.1	812	1	PLMS		A;Residues: 1-728 <SEK>
11	1379.5	33.4	812	1	PLMS		A;Cross-references: DDBJ:D90318
12	1371	33.2	810	1	PLHU		A;Residues: 1-728 <SE2>
13	1369	33.2	810	2	B30848		A;Cross-references: GB:M73239; NID:9337935; PIDN:AAA64239_1; PID:9337936
14	1333.5	32.8	810	2	I42260		R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
15	1212.5	29.4	4548	1	S00657		A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor.
16	1188.5	28.8	4120	2	A33869		A;Reference number: A41140; MUID:91334393
17	945	22.9	2669	2	T8518		A;Accession: A41140
18	818	19.8	460	2	B61545		A;Molecule type: mRNA
19	784.5	19.0	455	2	A61545		A;Residues: 1-728 <SE4>
20	559.5	13.6	559	1	A5029		A;Cross-references: EMBL:X16323
21	551.5	13.4	559	1	A29941		A;Experimental source: leukocyte
22	543	13.2	625	1	TBBO		R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nak
23	532.5	12.9	562	1	UKHUT		Biochem. Biophys. Res. Commun. 163, 967-973, 1989
24	531.5	12.9	618	2	A35827		A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth
25	527.5	12.8	622	1	TBHU		A;Reference number: A33512; MUID:89392017
26	518	12.6	617	2	S10511		A;Accession: A33512
27	510.5	12.4	603	2	S29491		A;Status: not compared with conceptual translation
28	480.5	11.6	655	1	A46688		A;Molecule type: mRNA
29	450	10.9	558	2	JCS878		A;Residues: 1-728 <MIY>

A; Cross-references: GB:M29145; NID:9184041; PID:9306846
 R; Rubin, J.S.; Chan, A.M.L.; Borttner, D.P.; Burgess, W.H.; Taylor, W.G.; Czech, A.C.; Hir
 proc. Natl. Acad. Sci. U.S.A., 88, 415-419, 1991
 A; Title: A broad spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte
 A; Reference number: A39006; MUID:9110540
 A; Accession: A39006
 A; Molecule type: mRNA
 A; Residues: 1-161, 167-728 <RUB>
 A; Cross-references: GB:M55379
 A; Experimental source: embryonic lung
 R; Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama,
 Biophys. Res. Commun., 175, 660-667, 1991
 A; Reference number: PH0114; MUID:91207365
 A; Molecule type: protein
 A; Residues: 32-43; 53-58 <YOS>
 A; Experimental source: plasma
 R; Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
 J. Cell. Biol., 111, 2108, 1990
 A; Title: Scatter factor: molecular characteristics and effect on the invasiveness of epithelial
 A; Reference number: A37796; MUID:91035621
 A; Molecule type: protein
 A; Residues: 86-91; 329-344; 356-363, 'XX', 366-370; 425-434; 442-447, 'X' 449-50; 543-546, 'X' 5
 R; Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashiro,
 Nature, 342, 440-443, 1990
 A; Title: Molecular cloning and expression of human hepatocyte growth factor.
 A; Reference number: 506794; MUID:90066676
 A; Accession: 506794
 A; Molecule type: mRNA
 A; Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'M', 301-316, 'A', 318-335, 'K', 337-386,
 A; Cross-references: EMBL:X16323; NID:932081; PID:CAA34387.1; PID:932082
 A; Experimental source: liver
 A; Note: the authors translated the codon CAG for residue 727 as Glu
 R; Hartmann, G.; Naldini, L.; Weidner, K.M.; Sacchi, M.; Vigna, E.; Comoglio, P.M.; Birchmeier,
 Proc. Natl. Acad. Sci. U.S.A., 89, 11549-11578, 1992
 A; Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth factor.
 A; Reference number: 159214; MUID:93087571
 A; Accession: 159214
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-288, 'ET', <HAR>
 A; Cross-references: GB:102931; NID:9184033; PID:AAA52649.1; PID:9184034
 R; Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
 Eur. J. Biochem., 197, 15-22, 1991
 A; Title: An alternatively processed mRNA generated from human hepatocyte growth factor.
 A; Reference number: SI5443; MUID:91200041
 A; Accession: SI5443
 A; Molecule type: mRNA
 A; Residues: 1-288, 'ET', <MYI2>
 A; Cross-references: EMBL:X557574; NID:932083; PID:CAA40802.1; PID:932084
 R; Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
 Biophys. Res. Commun., 180, 1151-1158, 1991
 A; Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
 A; Reference number: 152253; MUID:92062058
 A; Accession: 152253
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
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 A; Cross-references: GB:S62561; NID:9237996; PID:AAB20169.1; PID:9237997
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 A; Cross-references: GDB:127524; OMIM:142409
 A; Map position: 7q21.1-7q21.1
 A; Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 48
 C; Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C; Function: stimulates mitosis of hepatocytes and other cells
 A; Note: does not have protease activity
 C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology

C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
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 F;32-49/Domain: hepatocyte growth factor #status experimental <MAT>
 F;2-49/Domain: alpha chain #status experimental <ACH>
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 F;211-288/Domain: kringle homology <KR2>
 F;305-393/Domain: kringle homology <KR3>
 F;391-469/Domain: beta chain #status experimental <KR4>
 F;495-716/Domain: trypsin homology <TRY>
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 F;487-604/Disulfide bonds: #status predicted

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241	HRHFLPERYPDKGFFDDNCVCRNPDPGQPRPWPCYTLDPHTRWECYAIKTCADCNTMDTDVPL	QY	300	
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301	ETTCIQSOGEGYRGTYNNTIWINGIPQCQRDSDQYPTHEHDMTPENFKCOLRENYCRNPDG	Db	360	
301	ETTCIQSOGEGYRGTYNNTIWINGIPQCQRDSDQYPTHEHDMTPENFKCOLRENYCRNPDG	QY	360	
361	ESPMCFTTDPEPNTRVYGCSPONPCMDSHGODCYRNGKNMQLSQTSGLTCSMWDKME	QY	420	
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421	DLHRHFWEDASKLNENYCRNPDDAHPWCTGPNLPIPDWYCPISRCEGDTPTIVNL	QY	480	
421	DLHRHFWEDASKLNENYCRNPDDAHPWCTGPNLPIPDWYCPISRCEGDTPTIVNL	Db	480	
481	DHPVTSACKQLRKYVNGIPTRTNQGWMVSLRVNPKHTGGSLIKESWLTAQCPFSRD	QY	540	
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601	NYGCTTPEITSCSYGWGTYGLIWIWGLIRRAHYIMGNEKCSQHRRKVTESETAG	QY	660	
601	NYGCTTPEITSCSYGWGTYGLIWIWGLIRRAHYIMGNEKCSQHRRKVTESETAG	Db	660	
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A60185
 hepatocyte growth factor precursor - mouse
 N:Alternate names: hepatoprotein A; scatter factor
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1993 #sequence_revision:26-May-1994 #text_change:16-Jun-2000
 C:Accession: JC2117; PC2054; A60185; S43416; S45521; S17173; S10966; I18758; JU0231
 R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
 Biochem. Biophys. Res. Commun. 199, 772-779, 1994
 A:Title: Identification of mouse mammary fibroblast-derived mammary growth factor as hepatocyte growth factor
 A:Reference number: JC2117; MUID:94183257
 A:Accession: JC2117
 A: Molecule type: mRNA
 A: Residues: 1-1728 <SAS2>
 A:Cross-references: GB:D10212; NID:9220435; PIDN:BA001064.1; PID:9220436
 A:Experimental source: fibroblast; COS-1 cell
 A:Note: submitted to JIPID, May 1993
 A:Accession: PC2054
 A: Molecule type: protein
 A: Residues: 496-504 <SA2>
 R;Olsen, E.M.; Maromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.
 Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990
 A:Title: Purified scatter factor stimulates epithelial and vascular endothelial cell migration
 A:Reference number: A60185; MUID:90377927
 A:Accession: A60185
 A: Molecule type: protein
 A: Residues: 'X', 184-188, 'KX', 191-192, 'X', 194, 'XX', 197; 357-364, 'XX', 367; 375-377, 'E', 379, 'R'
 R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
 Biochim. Biophys. Acta 1215, 299-303, 1993
 A:Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth factor
 A:Reference number: S43416; MUID:94060105
 A:Accession: S43416
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1728 <LTU>
 A:Cross-references: EMBL:X72307
 R;Liu, Y.
 submitted to the EMBL Data Library, May 1993
 A:Reference number: S45521
 A:Accession: S45521
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1563, 'H', 565-728 <LTU>
 A:Cross-references: EMBL:X72307
 R;Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
 Biochem. J. 278, 35-41, 1991
 A:Title: Purification and characterization of biologically active scatter factor from rat liver
 A:Reference number: S17173; MUID:91354223
 A:Accession: S17173
 A:Molecule type: protein
 A: Residues: 496-517, 'T', 519 <COF>
 R;Gherardi, E.; Stoker, M.
 Nature 346, 228, 1990
 A:Title: Hepatocytes and scatter factor
 A:Reference number: S10966; MUID:9036152
 A:Accession: S10966
 A: Molecule type: preliminary
 A:Molecule type: protein
 A: Residues: 496-507, 'X', 509-512, 'L', 514-516, 'X', 518-519 <NAT>
 R;Plaschke-Schlueter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
 J. Biol. Chem. 270, 830-836, 1995
 A:Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
 A:Reference number: I18758; MUID:95122532
 A:Accession: I18758
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 C:Function:
 A:Description: stimulates mitosis of hepatocytes and other cells
 A:Note: does not have protease activity
 C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyridine nucleotide-binding protein domain; signal sequence

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QY	361 ESPFCFTDPNRPNGYCSQIPNCMDSHGQDGYCNGKNGMNSQTSRGLTCSMDKNE	420	420	420						
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QY	421 DLHRHIFWEPDASKLNENYCNRFDDDAHGPPWCUTGNPLIPWDYCPICRCEGDTPTIVNL	480	480	480						
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C;Species: Ratius norvegicus (Norway rat)	C;Accession: A35644; S12211	Db	362 ESPACFTTPNPINRKGYCSDIPKPCVQSSGCCDCCYRONGKNMGNLSKTRSGLTCMSWDKNE 421
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A;Residues: 1-728 <TAS>	A;Cross references: GB:90102; GB:M32987; NID:9220766; PIDN:BAAl4133_1; PID:9220767	Db	482 DHPVISCAKKQLKLRVNGITPTRTNIGWMSIRYRNKHCGS LIKESWLTAQCFSR- 541
A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417	R;Okajima, A.; Miyazawa, K.; Kitamura, N.	Qy	540 -DLKYEANGIIVHVGRODECKQVLNNSQLWGPESDDLVMLKARPAVLLDFVSTID 598
C;Keywords: alternative splicing; hepatocyte growth factor; kringle homology; trypsin homology; tyrosine kinase activity	F;1-32/Domain: signal sequence #status predicted <SIG>	Db	542 KDLKDYEWGIGIDHOVHGERGEKKRQLNLNSQLVYGPESDVLJLKLARPAILDNFVSTID 601
C;Superfamily: hepatocyte growth factor alpha chain #status predicted <MAT>	F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>	Qy	599 LPNIGCTPEKTSQSVYGMGTGLINYVGLRLVARYHLYINGNECSQHHRGKVYLNESEC 658
C;Function: stimulates mitosis of hepatocytes and other cells	F;12-29-207/Domain: kringle homology <KR1>	Db	602 LPSGCTTPEKTSQSVYGMGTGLINYVGLRLVARYHLYINGNECSQHHRGKVYLNESEC 661
A;Description: does not have proteinase activity	F;212-389/Domain: kringle homology <KR2>	Qy	659 AGAAKIGSGCPEGYGGPVCQEGHKMRMVLGVIVPGRCALPAIRPGCFIVRVAAYAKWIK 718
A;Note: the authors' translation for residue 70 is Gln, not GAC	F;306-384/Domain: kringle homology <KR3>	Db	662 AGAAKIGSGCPEGYGGPVCQEGHKMRMVLGVIVPGRCALPAIRPGCFIVRVAAYAKWIK 721
F;392-470/Domain: kringle homology <KR4>	F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>	Qy	719 ILIYKV 725
F;496-719/Domain: trypsin homology <TR>	F;293-403, 569, 656/Binding site: carbohydrate carboxylic acid (Gln) (in mature form) #status predicted	Db	722 VILTYKL 728
F;488-607/disulfide bonds: #status predicted			
Query Match 92.1%; Score 3802; DB 1; Length 728; Best Local Similarity 90.4%; Pred. No. 1.4e-259; Matches 657; Conservative 41; Mismatches 27; Indels 2; Gaps 1;	RESULT 4 151283		
Qy	1 MVTKLIPALLQVHLHLPLIAPIAEGRKRNTHERKKSAKTLRKIDPALKIK 60		hepatocyte growth factor precursor - clawed frog
Db	2 MWGTLKLPLVLLQHVHLHLPLIPTVIAEGOKKRNLHERKKSAKTLRKEDPLVKIK 61		N;Alternate names: hepatopietin A; scatter factor
Oy	61 TTKVNTADQCANRCTRKNGLPETCKAKVFDKARKQCLWPEPPNSMSSGVKKFGHEFDLYE 120		C;Species: Xenopus sp. (clawed frog)
Db	62 TTKVNSADECANRCIRKNGFPETCKAKVFDKRSRKCTWIPNSMSSGVKKFGHEFDLYE 121		C;Accession: 151283
Oy	121 NRDYIRNCIISGKRSYKGTVSTKSGKQPMSSMPHEHSLPLSSYRGKDLQLOVCRNP 180		R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
Db	122 NRDYIRNCIISGKRSYKGTVSTKSGKQPMSSMPHEHSLPLSSYRGKDLQLOVCRNP 181		Mech. Dev. 49, 123-131, 1995
Oy	181 RGEEGGPWCFTSNPVEYEVEDCPOSEVECMTCGESYRPMHDPESGKICQRWHOPT 240		A;Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus
Db	182 RGEEGGPWCFTSNPVEYEVEDCPOSEVECMTCGESYRPMHDPESGKICQRWHOPT 241		A;Reference number: 151283; MUID:95267690
Oy	241 HRHKFLPERYDKGDNYCNPDRGDPWYCAKIKCNSAVNDVPM 300		A;Accession: 151283
Db	242 HRHKFLPERYDKGDNYCNPDRGDPWYCAKIKCNSAVNDVPM 301		A;Status: preliminary
Oy	301 ETTECTIQOGQGEGYGRYNTVNTGIPQRWDSQYPHRHMTPENFKKDLRENYCRPDGS 360		A;Molecule type: mRNA
Db	302 ETTECTIQOGQGEGYGRYNTVNTGIPQRWDSQYPHRHMTPENFKKDLRENYCRPDGS 361		A;Residues: 1-728 <OKA>
Oy	361 ESPWCFTDPPIRVGVCSQLPNDMSHGQDCYRQNGKMYNLSQTRSGLTCMSMDKNE 420		C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
Query Match 68.0%; Score 2806; DB 1; Length 710; Best Local Similarity 66.1%; Pred. No. 1.5e-189; Matches 481; Conservative 107; Mismatches 120; Indels 20; Gaps 5;	RESULT 4 151283		
Qy	1 MVTKLIPALLQVHLHLPLIAPIAEGRKRNTHERKKSAKTLRKIDPALKIK 60		
Db	1 MWTKOMVIFLL-----ITLAEGRKKNRFAFDYKKAETTLRLNALEVK 47		
Qy	61 TTKVNTADQCANRCTRKNGLPETCKAKVFDKARKQCLWPEPPNSMSSGVKKFGHEFDLYE 120		

Db 48 TKMFNTENCARKCSRNRKGKLPFTCKAFADKNIKRCHWFSPNTMSAGIKDKYDISFDLYE 107
 Qy 121 NKDYIRNCITGKGRSYKGTVSITKSGIKCOPWSMMPHEHSFLPSSYRGKQLOENYCRNP 180
 Db 108 KKDYIRDCIHKGSNSYRGTRNVTKRGSLACOPWNNSMIPHEHSFLPSTYRGKDLKENYCRNP 167
 Qy 181 RGEEGGPWCFTSNPEVYEWCDIPQSEVECMTNGESYRGIMDHTESGKTCQRWDHQTP 240
 Db 168 KGEEGPWCFTSKPEYRHDVCDIPCESEDVCTNGEHYRGPMYKESKGRCQRMQLQRP 227
 Qy 241 HRHKFLPERYDGFDDNYCRNPDGSPRPWCYTLDPHTRWYCAIKTCADMNMNDTDPL 300
 Db 228 HKHFKFPERYFNKGNDNYCRNPDGKSRPWPWITLDPDTISWECFAIKPCVHSIVNNIDI- 285
 Qy 301 ETTEC1OQGEGYRGTVNTINGIPCORMDSQYPHRHMPPENFKDLRENYCRNPDGS 360
 Db 286 -TKDCMRQGEGYRGTVNTINGIPCORMDSQYPHLHNFTPENYKCKDLSENVCNRPDGS 344
 Qy 361 ESPWCFTTDPNRYGQCSQPNCDMSHGQDCYRGNGKMYGNLSQLTRSGLTCMSWDKNM 420
 Db 345 ESPWCFTTDPNTRIGHSQIKRKCQASNOQCYYGNGSTYKGTLSRFRFLPCSMWEKLNQ 404
 Qy 421 DLHRHFWEPDASKLUNENYCNPDDAAHGPWCYTGMLPUDYCPTSRCEGDTPTIVL 480
 Db 405 DLKRHFWEPDASKLUNENYCNPDDAAHGPWCYTGMLPUDYCPTSRCEGDTPTIVL 464
 Qy 481 DHPVTSACKTQLRVNGIPTRTICWMSLRYRNHICGSLIKESWVLJAROCFPRSR- 539
 Db 465 DSP-1TCSSSQQLRVRVNGIPTAKVWMSVRYRNHAKCGTLIKENWVLJAROCFLGD 523
 Qy 540 -DLKDEAWIGIHDMHGRGDEBKCKQVLNVSLVYGEPEGSDVLMLKARPAVLDDFVSTD 598
 Db 524 IDKYVEAWLGVHNTY-TEKKLQNTISOLVNLKSLRPAFTLAVYDRK 582
 Qy 599 LPNYGCTIPEKTSCSVYWGWTGLINYDGLLRLRAHIIYIMGNKECSOHHRGKVTLNESEIC 658
 Db 583 LPNYGCTIPEKTSCSVYWGWTGLINYDGLLRLRAHIIYIMGNKECSOHHRGKVTLNESEIC 642
 Qy 659 AGAKTGGPCEGDDGGPLYCEQKHMRVGLVTPRGCAIPNPGIFVRYAYAKWIHK 718
 Db 643 AIGETANIGPCERDYGGPLICEENRTHLVQGVITPGRGCAIQKRPVIFVRYAYAKWIHK 702
 Qy 719 TILTYKVP 726
 Db 703 IMLTYKAP 710

RESULT 5 151285

C;Species: Gallus gallus (chicken)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C;Accession: I51285
 R;Strait, A.; Stern, C.D.; Thary, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard Development 121, 813-824, 1995
 A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node during
 A;Reference number: 151285; MUID: 95237013
 A;Accession: I51285
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-411 <STR>
 A;Cross-references: GB:M74178; NID:9183976; PIDN:AAA50165.1; PID:9183977
 R;Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
 J. Biol. Chem. 268, 15461-15468, 1993
 A;Title: Cloning, sequencing, and expression of human macrophage stimulating protein
 A;Reference number: A47136; MUID:93340141
 A;Molecule type: mRNA
 A;Residues: 1-121 <HA2>
 A;Cross-references: GB:L11924; NID:939807; PIDN:AAA59872.1; PID:9398038
 A;Note: authors translated the codon TTT for residue 623 as Leu; parts of this sequence
 R;Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
 J. Exp. Med. 173, 1227-1234, 1991
 A;Title: Macrophage stimulating protein: purification, partial amino acid sequence, a
 A;Reference number: A61395; MUID:91217635
 A;Accession: A61395
 A;Molecule type: Protein
 A;Residues: 230-247; 288-291, 'E', 293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-310; 326-
 C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 F;1-24-197/Domain: kringle homology <KRG>
 F;20-27/Domain: kringle homology <KR>
 F;296-374/Domain: kringle homology <KR>

Query Match 44.1%; Score 1821.5; DB 2; Length 411;
 Best Local Similarity 73.7%; Pred. No. 1.4e-120;
 Matches 309; Conservative 49; Mismatches 52; Indels 9; Gaps 2;
 Qy 1 MWNTKLLPALLQHVLLLPIAIPYABGQKRRTNTIEFKSAKTTLIKIDPALKIK 60

Db 1 MWATOLLPLLLH---QLLPPITPAEAGKRRNPLHDYKKTGELMLIKVNKALEVK 56
 Qy 61 TKVNTADQCANRCTRNKGKLPFTCKAFADKNIKRCHWFSPNTMSAGIKDKYDISFDLYE 120
 Db 57 TKLNTTEQCARCSRNRKGKLSFTCKAFADKNIKRCHWFSPNTMSAGIKDKYDISFDLYE 116
 Qy 121 NKDYIRNCITGKGRSYKGTVSITKSGIKCOPWSMMPHEHSFLPSSYRGKQLOENYCRNP 180
 Db 117 KKDYVRNCITGKGAEVYGTISTIKSGIQCAWNNSMIPHEH----SYRKDLDRENYCRNP 171
 Qy 181 RGEEGGPWCFTSNPEVYEWCDIPQSEVECMTNGESYRGIMDHTESGKTCQRWDHQTP 240
 Db 172 RGEEGGPWCFTSQPMHEVCDIPSEVECMTNGESYRGIMDHTESGKSCQRWDQRP 231
 Qy 241 HRHKFLPERYDGFDDNYCRNPDGQPRPWCYTLDPHTRWEYCAIKTCADMNMNDTDPL 300
 Db 232 HKHFKFPERYDGFDDNYCRNPDGKURPWCYTLDPHTRWEYCAIKTCADMNMNDTDPL 291
 Qy 301 ETTEC1OQGEGYRGTVNTINGIPCORMDSQYPHRHMPPENFKDLRENYCRNPDGS 360
 Db 292 ETTEC1OQGEGYRGTVNTINGIPCORMDSQYPHLHNFTPENYKCKDLSENVCNRPDGS 351
 Qy 361 ESPWCFTTDPNRYGQCSQPNCDMSHGQDCYRGNGKMYGNLSQLTRSGLTCMSWDKNM 419
 Db 352 ESPWCFTTDPNTRIGHSQIKRKCQASNOQCYYGNGSTYKGTLSRFRFLPCSMWEKLNQ 410

RESULT 6 A47136

macrophage-stimulating protein 1 precursor - human

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_change 18-Jun-1999

C;Accession: A40331; B40331; A47136; A61395

R;Hahn, S.; Stuart, L.A.; Degen, S.J.F.

A;Title: Characterization of the DNFI5S2 locus on human chromosome 3: identification

A;Reference number: A40331; MUID: 92002016

A;Molecule type: DNA

A;Residues: 1-711 <HA1>

A;Cross-references: GB:M74179

A;Accession: B40331

A;Molecule type: mRNA

A;Residues: 1-711 <HA2>

A;Cross-references: GB:M74178; NID:9183976; PIDN:AAA50165.1; PID:9183977

R;Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.

A;Title: hepatocyte growth factor/scatter factor - chicken (fragment)

C;Accession: I51285

R;Strait, A.; Stern, C.D.; Thary, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard Development 121, 813-824, 1995
 A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node during
 A;Reference number: 151285; MUID: 95237013
 A;Accession: I51285
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-411 <STR>
 A;Cross-references: GB:L11924; NID:939807; PIDN:AAA59872.1; PID:9398038
 A;Note: authors translated the codon TTT for residue 623 as Leu; parts of this sequence
 R;Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
 J. Exp. Med. 173, 1227-1234, 1991
 A;Title: Macrophage stimulating protein: purification, partial amino acid sequence, a
 A;Reference number: A61395; MUID:91217635
 A;Accession: A61395
 A;Molecule type: Protein
 A;Residues: 230-247; 288-291, 'E', 293-295, 'X', 297-301, 'X', 303, 'E', 305, 'EX', 308-310; 326-
 C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C;Genetics:
 A;Gene: GDB:MST1; D3F15S2; DNFI5S2; HGFL
 A;Cross-references: GDB:128833; OMIM:142408
 A;Map position: 3p21-3p21.3
 C;Complex: disulfide bonded heterodimer of chains derived from the same precursor
 A;Experimental source: plasma
 C;Keywords: duplication; glycoprotein; growth factor; kringle; plasma
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-483/Domain: alpha chain #status predicted <ACH>

		F;110-186;/Domain: kringle homology <KR1>
		F;191-208;/Domain: kringle homology <KR2>
		F;283-361;/Domain: kringle homology <KR3>
		F;370-448;/Domain: kringle homology <KR4>
		F;484-711;/Domain: beta chain #status predicted <BCN>
		F;56-78, 60-65, 110-186, 131-169, 157-181, 191-268, 212-251, 240-263, 283-361, 304-343, 332-355, 37
		F;72, 296, 615;/Binding site: carbohydrate (Asn) (covalent) #status predicted
		Query Match 40.0%; Score 1652; DB 1; Length 711;
Matches	317;	Local Similarity 43.8%; Conservative 103; Mismatches 265; Indels 38; Gaps 14;
Qy	16	LLHILLPLIAPIAYEGORKRRTNTHEFKSKATTLTIKDPAKTK-TKKVNTADOCANR 73
Db	6	LLILITQYLGVP--GO---RSPLNDFOVLRGTEFLQHLHHAVVGPWQEDVADAECAGR 59
Qy	74	CTRIKGLPLPTCKAFVFDKARKQCWFPEPNMSSVKKGERHEEFLYENKYIRNCIGKG 133
Db	60	C---GPLMDCAFHYNSHSGCQLWPWTQHSRGRCDLFQKDYVRCTIMNG 115
Qy	134	RSYGTVSITKSGKCOPWSMIPHEHSLPSSYRKDQIENCRNPROBEGGWCFTSN 193
Db	116	VGVYGTMMATVGGIPLCQAMSHKFENDHKV-TPTLING--LEENFCRNPDGDPGGWCYTID 173
Qy	194	PEVRYEVCDIPQCSVEECMTCMTGNGSYRGLMDHTSSESGKICQRWDHQTPHRHKFLPERYDK 253
Db	174	PAVRFQSCGIKSCKRACAYCWNGEYRGAVDRTRSGRECQRCWRDQHOPHOPFEGKFLDQ 233
Qy	254	GDFDNYCRAPIRDGDRPRCPCTLDPTPRWECAIKTCADNTMDTIVPLETTECTCGOGEGY 313
Db	234	GLDNYCRNEDGDSRPWCYTDPTDQIREFCDLPRGSSEAPROFA--TVVSCFRGKGEY 291
Qy	314	RGTNTINTWINGIPCCRDPSOYSPHEEDMTPEFKCDLREWCNRDGSESPWCFTDPNIR 373
Db	292	RGTANTTTAGVPCPCRWDAGIIPHQRFTPERYACKDLRENFCRNPDGSEAPWCFTLRPGMR 351
Qy	374	VGYQSQIPNC-DMSHGQDCYRGNGKNYMGNLISQTRSGLTCSMWDKNMDLHRHFWEPDA 432
Db	352	AAFCQYQIRRCTDPYRQPQDGYHAGEBQYRGHVSKTRKGVQDCORMWAETPHKPQFTTSEPH 411
Qy	433	SKLNENYCRNPDHDGPGWCYTGPNLIPWQYCP-SRCEGDTPTPVNLDPH--VISCA 488
Db	412	AQLEENFCRNPDGDSHPGWCYTMDDPRTPDFCALRNCADDQPSI-LDPPDQWQFEKCG 469
Qy	489	K-----TKQLRVNGIPTRTNGWMSLRYR-NKHICGSLIKESWLTAROCFS - 538
Db	470	KVRDLDORRSKLRTVGGHP--GNSPWTYSLRNROGQHFCGSSLVKEQWLTATAROCFSSC 527
Qy	539	-RDKDYEAWLGHIDVHGRDKEKKVQLVNLNSQLYGPGEGSDLVMLKLRAPAVLDDFVSTI 597
Db	528	HMPLTGYEWNLGTLFQNPOHQEPSLQRVPAKMCVGPSSQSLVWKLERSVTNLNOMVALI 587
Qy	598	DLPNYGCTIPEKTSOSVYGMGTYGLINVDOLLRWHALYMGNEKCSQHHRGVLTNESEI 657
Db	588	CLPPPEWYVPPGKCEIAGMGETKGNTDVLNLNALLNVISNQECNIKKGKV--RESEM 645
Qy	658	CAGAEKIGKSPCECGYGGPLVCEQHMKMVLGLVIVPGRCGAIPNRPQIFYRVAYAKWIH 717
Db	646	CTEGLLAPVGACESDYGGLPLACTHNCWVLEGITIPNRCARSRNPAVFTRSVFVDWIH 705
Qy	718	KII 720
Db	706	KVM 708
RESULT	7	
JC5061		macrophage-stimulating protein 1 precursor - rat
C;Species:		Rattus norvegicus (Norway rat)
C;Accession:		31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
A;Cross references:		EMBL; X95096; NID:91669718; PID:CAA64473.1; PID:91669719
A;Complex:		disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily:		hepatocyte growth factor
C;Keywords:		duplication; glycoprotein; growth factor; kringle homology; trypsin homology
A;Reference number:		JC5061; MUID:97011126
A;Accession:		
A;Molecule type:		mRNA
R;Oshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu Biochem. Biophys. Res. Commun. 227, 273-280, 1995		
A;Title:		Molecular cloning of rat macrophage-stimulating protein and its involvement
F;32-488;/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <SIG>		
F;32-488;/Product: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>		
F;110-186;/Domain: kringle homology <KR1>		
F;191-208;/Domain: kringle homology <KR2>		
F;283-361;/Domain: kringle homology <KR3>		
F;370-448;/Domain: kringle homology <KR4>		
F;484-711;/Domain: beta chain #status predicted <BCN>		
F;56-78, 60-65, 110-186, 131-169, 157-181, 191-268, 212-251, 240-263, 283-361, 304-343, 332-355, 37		
F;72, 296, 615;/Binding site: carbohydrate (Asn) (covalent) #status predicted		
A;Residues:		1-716 <CYS>
C;Cross references:		EMBL; X95096; NID:91669718; PID:CAA64473.1; PID:91669719
C;Complex:		disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily:		hepatocyte growth factor
C;Keywords:		duplication; glycoprotein; growth factor; kringle homology; trypsin homology
F;31;/Domain: signal sequence #status predicted <SIG>		
F;32-488;/Product: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>		
F;110-186;/Domain: kringle homology <KR1>		
F;191-208;/Domain: kringle homology <KR2>		
F;283-370;/Domain: kringle homology <KR3>		
F;370-457;/Domain: kringle homology <KR4>		
F;483-716;/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCN>		
F;483-709;/Domain: trypsin homology <TRY>		
F;72, 305, 620;/Binding site: carbohydrate (Asn) (covalent) #status predicted		
Query Match 39.1%; Score 1615; DB 1; Length 716;		
Best Local Similarity 43.3%; Pred. No. 8.6e-106; Matches 315; Conservative 118; Mismatches 254; Indels 40; Gaps 16;		
Qy	17	LHLILITPIAYEGORKRRTNTHEFKSKATTLK-TDPAKTK-VNTADOCANR 74.
Db	4	LPLLLAQQSRLAQGQ--RSPLNDFQELLRGTEFLNLHPLVYVPGWQEDVADAECARCK 60
Qy	75	TRNKGLPFTCKAFVFDKARKQCWLWFPNSMSSGVKREFGEHEDLYENKYIRNCIGKG 134
Db	61	--GPLLDRCAFRAHYNMSSGCOLLPWTQHSRDLAQHHSCLDQKQDVYDABECARCK 60
Qy	135	SYKGVISITSGIKQPMWSMIPHEHSFLSSYRQKDLQNYCNPURGPRGBGGPQFTSN 194
Db	117	SYRGTAVTADGLPQAWSRFPNPKYTPPTKNG--LEENFCRNPDGDPGPRGPWCYTTR 174
Qy	195	EVRYEVCDIPOCSEECMTCMTGNGSYRGLMDHTESSESGKICQRWDHQTPHRHKFLPERYDK 254
Db	175	SVRFQSGCGINSCREAVCQWNGEDYRGEVYTESRECQWDQLQPHSHPFPEKDKA 234
Qy	255	FDDNYCRRNPDCPQCPRPWCYTDPLPHTREYCAIKTCADN----TMNDTIVPLETTECTQ 307
Db	235	LKDNYCRNPDASPERWCYTDPVNVEREFCDFLPSCPGSLNPPTKGSKSQRNKAASNCFR 294
Qy	308	QGEGYGRGTTWNTIWCIPCQWHDQSPHEEDMTPEFKCDLREWCNRDGSESPWCFT 367
Db	295	GKGDYDRTGTTNTTSAGVPCORWDAONPHRVPYACKDLRENFCRNPDGSEAPWCFT 354
Qy	368	TDPNRYGQSQIPNC-DMSHGQDCYRGNGKNYMGNLISQTRSGLTCSMWDKNMDLHRH 426
Db	355	SRPGLRVAFCQVQIPRTEEVVPEVPGCYHSQSRQYRGSVSKTRKGVQCOHW--SSENPHPK 412
Qy	427	FWEPDA--SKLNENYCRNPDHDGPGWCYTNPLPWCYDPCISRCGDTPTIVNLDPH 484
Db	413	FTPTSAFHGLEAFNCRNPDGDSHPGWCYTDPLPTEFLDYCALRKCDQDQPSI-LDPPY 470
Qy	485	---ISCAK---TKQLRVNGIPTRTNGWMSLRYR-NKHICGSLIKESWLTAROC 535
Db	471	QVQFERKGVYDOSNRLRVYQGK--GNSPWVTSRNRQHFCGGLVKBOWLTAROC 528
Qy	536	FPS---RDLKDYAWLGHIDVHGRDKCKQVUNLNSOLVYQGPGESDIVLMLKLRAPVLDFF 593
Db	529	IWSCHDPLTGYEWNLGTLINQNPQGPBANLQRVSVAKTVCQGSQLVLIKERVITNH 588
Qy	594	VSTIDLQNYGCTIPEKNSCISYWGTYTGLINVDGLLRAHYIMGNEKCCSOHHRKVTLN 653
Db	589	VARICLUPEQYVVPGPCTEAGMGETKGNTDVLNLNALLNVISNQECNIKKGKV--Q 646
Qy	654	ESEIAGAEKIGKSPCECGYGGPLVCEQHMKMVLGLVIVPGRCGAIPNRPQIFYRVAYA 713

P;561-783/Domain: trypsin homology <TRY>
 F;30-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
 bonds: #status Predicted
 C;Active site: His, Asp, Ser #status predicted

Query Match 35.1%; Score 1446.5; DB 1; Length 790;
 Best Local Similarity 35.9%; Pred. No. 6.8e-94;
 Matches 294; Conservative 114; Mismatches 232; Indels 157; Gaps 20;
 C;Accession: S45046; A;Molecule type: mRNA
 A;Residues: 1-812 <BER>

A;Cross-references: EMBL:X79402; NID:9494962; PIDN:CAA55939.1; PID:9494963

A;Experimental source: Liver

A;Note: it is uncertain whether Met-1 or Met-8 is the initiator

R;Schaller, J.; Moser, P.W.; Danner-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; R

Eur. J. Biochem. 149, 267-278, 1985

A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human pl

A;Reference number: A25835

A;Accession: A25835

A;Molecule type: Protein

A;Residues: 27-34, D', 336-515, H', 517-554, L', 556-812 <SCH>

R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A;Title: Characterization of a complementary deoxyribonucleic acid coding for human a

A;Reference number: I45961; MUID:8502331

A;Accession: I45961

A;Status: translated

A;Molecule type: mRNA

A;Residues: 706-743, R', 745-812 <MAL>

A;Cross-references: GB:K02915; NID:gi163551; PIDN:AA30714.1; PID:gi163552

R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lerger, W.; Manneberg,

Eur. J. Biochem. 114, 465-470, 1981

A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

A;Reference number: S03735; MUID:81212097

A;Accession: S03735

A;Molecule type: protein

A;Residues: 27-83 <BRU>

A;Function:

C;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a

on the walls of the graafian follicle; also activates the urokinase-type plasminogen

A;Pathway: fibrinolysis

C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol

C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kringle; plas

F;1-26/Domain: signal sequence #status predicted <SGT>

F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>

F;27-812/Product: plasminogen #status experimental <PRO>

F;27-103/Domain: activation peptide #status experimental <APT>

F;104-583/584-812/Product: plasmin #status experimental <AP1>

F;104-188/Domain: plasmin chain A #status experimental <ACH>

F;197-269/Domain: kringle homology <KR2>

F;282-359/Domain: kringle homology <KR4>

F;484-461/Domain: kringle homology <KR5>

F;584-812/Domain: plasmin chain B #status experimental <BCB>

F;584-805/Domain: trypsin homology <TRY>

F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342

bonds: #status predicted

F;365/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental

F;624,667-762/Active site: His, Asp, Ser #status predicted

Db 713 EYLGGGVSPN--ELCAGHLAGGIDSCQGDGGPLVCFEKDVKYLOGVTSGNGCALPNKP 770

Query Match 34.1%; Score 1408.5; DB 1; Length 812;

Best Local Similarity 35.4%; Pred. No. 3.3e-91;

Matches 280; Conservative 117; Mismatches 240; Indels 155; Gaps 15;

C;Accession: S45046; A;Molecule type: mRNA

A;Residues: 1-812 <BER>

A;Cross-references: EMBL:X79402; NID:9494962; PIDN:CAA55939.1; PID:9494963

A;Experimental source: Liver

A;Note: it is uncertain whether Met-1 or Met-8 is the initiator

R;Schaller, J.; Moser, P.W.; Danner-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; R

Eur. J. Biochem. 149, 267-278, 1985

A;Title: Complete amino acid sequence of bovine plasminogen. Comparison with human pl

A;Reference number: A25835

A;Accession: A25835

A;Molecule type: Protein

A;Residues: 27-34, D', 336-515, H', 517-554, L', 556-812 <SCH>

R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.

Biochemistry 23, 4243-4250, 1984

A;Title: Characterization of a complementary deoxyribonucleic acid coding for human a

A;Reference number: I45961; MUID:8502331

A;Accession: I45961

A;Status: translated

A;Molecule type: mRNA

A;Residues: 706-743, R', 745-812 <MAL>

A;Cross-references: GB:K02915; NID:gi163551; PIDN:AA30714.1; PID:gi163552

R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lerger, W.; Manneberg,

Eur. J. Biochem. 114, 465-470, 1981

A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

A;Reference number: S03735; MUID:81212097

A;Accession: S03735

A;Molecule type: protein

A;Residues: 27-83 <BRU>

A;Function:

C;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a

on the walls of the graafian follicle; also activates the urokinase-type plasminogen

A;Pathway: fibrinolysis

C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol

C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kringle; plas

F;1-26/Domain: signal sequence #status predicted <SGT>

F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>

F;27-812/Product: plasminogen #status experimental <PRO>

F;27-103/Domain: activation peptide #status experimental <APT>

F;104-583/584-812/Product: plasmin #status experimental <AP1>

F;104-188/Domain: plasmin chain A #status experimental <ACH>

F;197-269/Domain: kringle homology <KR2>

F;282-359/Domain: kringle homology <KR4>

F;484-461/Domain: kringle homology <KR5>

F;584-812/Domain: plasmin chain B #status experimental <BCB>

F;584-805/Domain: trypsin homology <TRY>

F;56-80,60-68,110-188,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342

bonds: #status predicted

F;365/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;365/Binding site: carbohydrate (Ser) (covalent) #status experimental

F;624,667-762/Active site: His, Asp, Ser #status predicted

Db 704 GIFVRVAYAKWIKHII 720

Query Match 34.1%; Score 1408.5; DB 1; Length 812;

Best Local Similarity 35.4%; Pred. No. 3.3e-91;

Matches 280; Conservative 117; Mismatches 240; Indels 155; Gaps 15;

C;Accession: S45046; A;Molecule type: mRNA

A;Residues: 1-812 <BER>

A;Cross-references: EMBL:X79402; NID:9494962; PIDN:CAA55939.1; PID:9494963

A;Experimental source: Liver

A;Note: it is uncertain whether Met-1 or Met-8 is the initiator

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A;Accession: A25835

A;Molecule type: Protein

A;Residues: 27-34, D', 336-515, H', 517-554, L', 556-812 <SCH>

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A;Accession: I45961

A;Status: translated

A;Molecule type: mRNA

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A;Cross-references: GB:K02915; NID:gi163551; PIDN:AA30714.1; PID:gi163552

R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lerger, W.; Manneberg,

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A;Accession: S03735

A;Molecule type: protein

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A;Function:

C;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a

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A;Pathway: fibrinolysis

C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homol

C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kringle; plas

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Db 771 GVYVRVSRFVWIEEIM 787

Query Match 34.1%; Score 1408.5; DB 1; Length 812;

Best Local Similarity 35.4%; Pred. No. 3.3e-91;

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C;Accession: S45046; A;Molecule type: mRNA

A;Residues: 1-812 <BER>

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A;Experimental source: Liver

A;Note: it is uncertain whether Met-1 or Met-8 is the initiator

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A;Reference number: A25835

A;Accession: A25835

A;Molecule type: Protein

A;Residues: 27-34, D', 336-515, H', 517-554, L', 556-812 <SCH>

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A;Title: Characterization of a complementary deoxyribonucleic acid coding for human a

A;Reference number: I45961; MUID:8502331

A;Accession: I45961

A;Status: translated

A;Molecule type: mRNA

A;Residues: 706-743, R', 745-812 <MAL>

A;Cross-references: GB:K02915; NID:gi163551; PIDN:AA30714.1; PID:gi163552

R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lerger, W.; Manneberg,

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A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma

A;Reference number: S03735; MUID:81212097

A;Accession: S03735

A;Molecule type: protein

A;Residues: 27-83 <BRU>

A;Function:

C;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a

on the walls of the graafian follicle; also activates the urokinase-type plasminogen

A;Pathway: fibrinolysis

Db 456 ETGGSSWEL--PTVSQEPSPGSDSETDCMVGNGKDYRGKTAVTAGTPCOGWAQEPHRH 513
 Qy 487 -----CAKTKQL----- 493
 Db 514 SIFPQTNPRADEKKNYCRNPDGQVNGPWCYTHPRKLVDYCDIPLCASASSEFCGKPOV 573
 Qy 494 -----RVNG--IPTRTNIGWMWMSLRYR--NKHCGGSLIKESWVLTARQCFFPSRDLKD 543
 |||| v : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 574 EPKPKPGPGRVYWGCVANPHSWPWOISLRTRPTGQHFCGGPLIAPSWKLTAAHCLKKSRPE 633
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Qy 544 -YEWLGIHDVHGIGDECKQVLNLNSQLVYGPESDLDVLMKLAERAVLDFVSTDLPNY 602
 | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 634 FYKVILGANHEEYIQLD--VQEISVAKLLEPNNRDIALKLSPATIDTKVPAICLPPS 691
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Qy 603 GCTTPEKTCGCSVWKGWTGLINVGLRLYAHLYMGNEKCSOHRGKVTLNESITCAGAE 662
 ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 692 NYMWADRTICYITQWGETQTFGAGRLKEAQOLPVVIENKVCNRVEYLNNRVKSTELCAGOL 751
 | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Qy 663 KIGSGPCEDYGGGLVUCEQHKMRMLVLYVPGRCALIPNRPGRITVRYVAYAKWHR 718
 | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
 Db 752 AGGVDSQCGDGGPLVCFDKYIQLQVTSWGLGCARPNKPGVYVVRVSRFDWLER 807
 | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

RESULT 12

PLHU

Plasmin (EC 3.4.21.7) precursor [validated] - human

N; Contains: angiotensin; microplasmin; plasminogen

C; Species: Homo sapiens (man)

C; Date: 24-APR-1984 #sequence-revision 02-Dec-1994 #text-change 15-Sep-2000

C; Accession: A35229; I5242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A04622; A04621; A04620; A04624; A04623; A04626; A04628; A04629; A04625; A04626; A04627; MUID:7722545

A; Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <5OT>

R; Wiman, B.

Bur. J. Biochem. 76, 129-137, 1977

A; Title: Primary structure of the B-chain of human plasmin.

A; Reference number: A04627; MUID:7722545

A; Accession: A04627; MUID:75093329

A; Molecule type: protein

A; Residues: 581-810 <W1L>

R; Wiman, B.; Wallen, P.

Eur. J. Biochem. 50, 489-494, 1975

A; Title: Structural relationship between "glutamic acid" and "lysine" forms of human

A; Reference number: A04625; MUID:75093329

A; Accession: A04625

A; Molecule type: protein

A; Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <W12>

R; Wiman, B.; Wallen, P.

Eur. J. Biochem. 58, 539-547, 1975

A; Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen

A; Reference number: A04626; MUID:76043692

A; Accession: A04626

A; Molecule type: protein

A; Residues: 483-507, 'E', 509-604 <W13>

R; Robbins, K.C.; Arzadon, L.; Summaria, L.

J. Biol. Chem. 248, 1631-1633, 1973

A; Title: The primary structure of human plasminogen. II. The histidine loop of human

A; Reference number: A92125; MUID:3149248

A; Contents: annotation; active site

R; Groskopf, W.R.; Summaria, L.; Robbins, K.C.

J. Biol. Chem. 244, 3590-3597, 1969

A; Title: Studies on the active center of human plasmin. Partial amino acid sequence of the C-terminal portion of the molecule

A; Reference number: A92048; MUID:69234739

A; Contents: annotation; active site

R; Trexler, M.; Vali, Z.; Parthy, L.

J. Biol. Chem. 257, 7401-7406, 1982

A; Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen

A; Reference number: A9282; MUID:8221905

A; Contents: annotation; omega-aminocarboxylic acid binding sites

R; Vahl, Z.; Parthy, L.

J. Biol. Chem. 259, 13690-13694, 1984

A; Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin binding

A; Reference number: A92458; MUID:85054794

A; Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site

R; Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehnle, S.; McCance, S.

J. Biol. Chem. 271, 29461-29467, 1996

A; Reference number: A58811; MUID:97067211

A; Contents: annotation

R; Tuulins, A.; Mulchak, A.M.

R; Lijnen, H.R.; Uguru, F.; Bini, A.; Collen, D.

Biochemistry 37, 4699-4702, 1998

A; Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1

A; Reference number: A51341; PDB:1PK4

A; Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454

R; Tulinsky, A.; Wu, T.P.

A; Status: submitted to the Brookhaven Protein Data Bank, July 1991

A; Reference number: A51488; PDB:2PK4

A; Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454

R; Wu, T.P.; Tulinsky, A.

R; Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;

Db	799	: :::	Qy	433	-----SKLENWCNRNPDAAHGPWCYTGNPLPWCYPISRCEGDTTPTVNLDPV
RESULT	13		Db	516	FTPETNPRAGLEKNCRNPDDGPGVGPCTTNPRLFDYDVFQCAASS-----
B30848			Qy	485	ISCAKTK - ---QLRVWV-IPRTNTGWMVMSLYR-NKHCGSLLKESWLTAOCF
plasmin (EC 3.4.21.7) precursor - rhesus macaque			Db	565	FDCGKPOVEPKKCGRVGCVAVPHSMWPQISLURTRLGMFCCGTLSPEWLTAAHL
C;Species: Macaca mulatta (rhesus macaque)			Qy	537	PSDLKD-YEWLGH-DVHGRCDECKOVLNTSOLVGGPESDLVIMKLARPAVLDFV
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999			Db	625	EKSRSRSPFVKVILGAHREV- -LEPHVQETEVSKMFSERADIALLKSSPAITDKV
R;Tomlinson, J.E.; McLean, J.W.; Dawn, R.M.			Qy	595	STIDLPPNGCTIPKTSQVYGMGTGLINQDGELRVLAHYIMGNEKCSQHHRGVVLNE
J. Biol. Chem. 264, 5955-5965, 1989			Db	682	IPACLPSPMVVADRTCEFTITGWCTGTCGTOQTYAGLILKEARPLVYCNRYEFLNGTVKT
A;Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.			Qy	655	SEICAGAEKIGSCPEGYGLVCEQIKRMVLMGVITVGRGAIPNPGIFWRVAYAK
A;Reference number: A32869; MUID:89174660			Db	742	TELCAGHLAGGTBSCQGDSSGGLPVCFERDKYIILQGVTSWGLGCARPMPKGIVVRSRFV
A;Status: preliminary			Qy	715	WIHKII 720
A;Molecule type: mRNA			Db	802	WIEGM 807
A;Residues: 1-810 <TR>			RESULT	14	
A;Cross-references: GB:J04697; NID:g342272; PID:AAA36901.1; PID:g342273					
C;Superfamily: plasmin; kringle homology <KR3>					
F:377-354/Domain: plasminogen-related protein precursor homology					
F:481-560/Domain: kringle homology <KR5>					
F:581-803/Domain: trypsin homology <TRY>					
F:49-73-53-61,103-124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,32					
F:622,665,760/Active site: His, Asp, Ser #status predicted					
Query Match	33.2%	Score 1369; DB 2;	Qy	433	-----SKLENWCNRNPDAAHGPWCYTGNPLPWCYPISRCEGDTTPTVNLDPV
Best Local Similarity	33.8%	Length 810;	Db	516	FTPETNPRAGLEKNCRNPDDGPGVGPCTTNPRLFDYDVFQCAASS-----
Matches	286;	Conservative 127; Mismatches 257; Indels 176; Gaps 21;	Qy	485	ISCAKTK - ---QLRVWV-IPRTNTGWMVMSLYR-NKHCGSLLKESWLTAOCF
Qy	12	LQHVLLHLLPLIAPIPAAEGOKRRNNTIHEFKSKAKTTLIKDPALKIKTK--VNTAD 68	Db	565	FDCGKPOVEPKKCGRVGCVAVPHSMWPQISLURTRLGMFCCGTLSPEWLTAAHL
Db	1	MENKEVVLILL-LFLKSGOGE----PLDDVYNTKGASLFSI-----TKQLAGSIE 47	Qy	537	PSDLKD-YEWLGH-DVHGRCDECKOVLNTSOLVGGPESDLVIMKLARPAVLDFV
Qy	69	OQANCRTRNKGFLPTCAFKVARKQCLWFENNSMSGVKREFHGFEDILENKDYIRNC 128	Db	625	EKSRSRSPFVKVILGAHREV- -LEPHVQETEVSKMFSERADIALLKSSPAITDKV
Db	48	ECAAKEEE - EFTCRSFQHHSKEQQCIVMAENRKSSIVFRM--RDVVLFEKKVILSEC 103	Qy	595	STIDLPPNGCTIPKTSQVYGMGTGLINQDGELRVLAHYIMGNEKCSQHHRGVVLNE
Qy	129	TIGKGRSYKGVTSITSGIKCOPWSSMIPHEINSFLSSYRQKDQENYCRIPRGEGGPW 188	Db	682	IPACLPSPMVVADRTCEFTITGWCTGTCGTOQTYAGLILKEARPLVYCNRYEFLNGTVKT
Db	104	KTGNGKIRGKIRGMSKIRGITQKWSSTSIPRHTSPATHPSBGELEENYCRNPDNDQSQPW 163	Qy	655	SEICAGAEKIGSCPEGYGLVCEQIKRMVLMGVITVGRGAIPNPGIFWRVAYAK
189	CFTSNPVERYEVCDIPOCSEVCMTCNGESYRGLMHTESSKICQRMHDQTPHRKFLPE 248	Db	742	TELCAGHLAGGTBSCQGDSSGGLPVCFERDKYIILQGVTSWGLGCARPMPKGIVVRSRFV	
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Qy	249	RYPDKFEDDNQCRNPQPRCWCYIPLDPTWAEYKAKTCADNTMNDTIVDYLE- -FTECI 306	Db	802	WIEGM 807
Db	223	KFPNKNLKKNNCRNPDPGEPRPWCFTTDPNKWELCDIPRT----TPPSGSPYQCL 276	RESULT	14	
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Db	277	KGTGEWYRGDVAWTSGHTCIGMSAQTPHTNRPENFKLDENCFCRNPDGSESPWC 336			
Qy	367	TTDPLNIRVYGCQINPCDMSH-----GDCYRNGKNTMGNSQTRSG 409			
Db	337	TTNSQVRWEFC-KIRSCCESSPVSTPLDPTTAPPELTIPVWVOCYHGDGOSYRGQTSSMTTG 395			
Qy	410	LTCWSWDKNEDLHR-----HME----- 429			
Db	396	KKCQSWSSMTPHWHKTPENPNAGLTMNYCRNPDPADKGPMWCFTTDPSPVREYCNLKKC 455			
Qy	430	-----PDA----- 432			
Db	456	GTEGSVAAPPVVAQPLPDAETPSEEDCMFGNGKGVKGKAKTIVTGIPCQEAQAOEPHSRI 515			
Query Match	32.8%	Score 1353.5; DB 2;	Qy	433	-----SKLENWCNRNPDAAHGPWCYTGNPLPWCYPISRCEGDTTPTVNLDPV
Best Local Similarity	35.1%	Length 810;	Db	516	FTPETNPRAGLEKNCRNPDDGPGVGPCTTNPRLFDYDVFQCAASS-----
Matches	277;	Conservative 110; Mismatches 255; Indels 147; Gaps 16;	Qy	485	ISCAKTK - ---QLRVWV-IPRTNTGWMVMSLYR-NKHCGSLLKESWLTAOCF
Qy	61	TKK--VNTADQCANRCTRNGFLPTCKAFVFDKARKQCLWFENNSMSGVKKEFGERD 117	Db	565	FDCGKPOVEPKKCGRVGCVAVPHSMWPQISLURTRLGMFCCGTLSPEWLTAAHL
Db	37	TKQLSVGSTRECAYKC---EETSFICRSFQHHSKEQQCIVMAENKSFKIVLRM--RDV 92	Qy	537	PSDLKD-YEWLGH-DVHGRCDECKOVLNTSOLVGGPESDLVIMKLARPAVLDFV
Qy	118	LYENKQYTRNCNGKRSYKVTSTKSGKICOPSSMITHEHSLPLSSYRKGQDQENYC 177	Db	625	EKSRSRSPFVKVILGAHREV- -LEPHVQETEVSKMFSERADIALLKSSPAITDKV
Db	93	LPEKKMLSECKVGNGYRQYRTVSKTGTQKQSAETPHKPRFSPDENSEGIDQNYC 152	Qy	595	STIDLPPNGCTIPKTSQVYGMGTGLINQDGELRVLAHYIMGNEKCSQHHRGVVLNE
Qy	178	RNPREGEGGPWCFTSPEWVWVCIPOCSEVCMTCNGESYRGLMDHESKGICQRWDH 237	Db	682	IPACLPSPMVVADRTCEFTITGWCTGTCGTOQTYAGLILKEARPLVYCNRYEFLNGTVKT
Db	153	RNPDPDKGPWCYMDPEVRYEYCEIQC-EDECHMCSCONYVGRISRMGLCQPMWS 211	Qy	655	SEICAGAEKIGSCPEGYGLVCEQIKRMVLMGVITVGRGAIPNPGIFWRVAYAK
Qy	238	QTPHRKFLPERPYDKGFDNYCRNPDPADKGPMWCFTTDPSPVREYCNLKKC 297	Db	742	TELCAGHLAGGTBSCQGDSSGGLPVCFERDKYIILQGVTSWGLGCARPMPKGIVVRSRFV
Db	212	QIPHPHQFISKFPSKLNKANCRNPDPADKGPMWCFTTDPSPVREYCNLKKC 265	Qy	715	WIHKII 720
Qy	298	VPLE--TTECTIOGQGEGYRSTVNTIWNGIPCQQRWDSQYPHEHDMPENFKCDLRENCFCR 355			

Db	266 PPPSGPTOCLMGEHFOGNVAVTWSGLTCRGEOQSPHRHDRTPEIPCKNLDENYCR	Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
Qy	356 NPDGSESSPWCFTDPUPTNTRVGCSCIPNC-----DSMHG-----	A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipoprotein(a) gene
Db	326 NPDCPAPCFCFTTNSVSRFC-KIPDCVSSASERHSADPAVTPVPEOTPVWQBCYQENG	A;Reference number: A47233; MRID:93087573
Qy	419 -----	A;Accession: 16096
Db	445 SVRWEFCNLKKCGSTEMSATNSPPVQVSASESSESSEQDIDNGKGYRGTKATGGAGTPCQ	A;Status: preliminary; translated from GB/EMBL/DDBJ
Qy	419 --MEDLRRHIFWPPDA--SKINENYRNPDDDAHGPMWCYTNPLIMWDYCPIPSRCBD	A;Molecule type: DNA
Db	385 QTYVGTSSSTITGKQCQPTSMRPRHRSKTPENYPDADLMNYCORNPGDKGPWCYTDP	A;Residues: 1-16 <REB>
Qy	419 -----	A;Cross-references: GB:M90078; NID:9178786; PIDN:AAA35547.1; PID:9553188
Db	473 TPPTIVNLDPHPVTCASKRQLRVNGIPTRTNIGMWSLRVNRKHCIGSLIKESWLTA	R;Ichinose, A.
Db	562 VSPRSADCGKPKVPEKKPG-RVGGCVAMPHSPWQSVLREGCHFCGGTLISPEWVITA	Biochemistry 31, 3113-3118, 1992
Qy	533 RQCFPS-RDLKDVEAWLGHDVINGRGDERCKQVINVSQLVYGGFEGSDIVLMKLARPAVID	A;Accession: A47233
Db	621 AHCLEKEFSRPAIKVWLGAHQETRL-ERDVQIKGVTRKMLEPYRADLALKLSSPAIT	A;Title: Multiple members of the Plasminogen-apolipoprotein(a) gene family associated with the fibrinolytic system
Qy	592 DFVSTIDLPNYGCTTPEKUSCSTYVGWGYGLINDGLURVAHYIMGEJEKCSQHHRGKV	A;Reference number: 152415; MRID:92207924
Db	679 DKDIFACILNSNVNAVDISLCYTGWGEGRKGTGAGLIRKAOLFVIENKVNQNSFLNGR	A;Accession: 152415
Qy	652 LNESEICAGAEGKIGSGPCEGDDYGGPLVCEQHKMRMLVYIVPGRGCAIPNRPGLFVRYAY	A;Status: preliminary; translated from GB/EMBL/DDBJ
Db	739 VRSPELCAHGHLAGCVDSCQGDGSPGLVCFEKDRYILOGVTSMWGLCARLITRPGVYVRVSR	A;Note: apo(a) gene 1 (nomenclature of reference 152415)
Qy	712 YAKWIHKII 720	A;Accession: 162867
Db	799 YVSMIQLQDMV 807	A;Residues: 1-16 <REB>
RESULT	15	A;Cross-references: GB:M86878; NID:9178782; PIDN:AAA51749.1; PID:9553186
S00657	apoliprotein(a) (EC 3.4.21.-) precursor [validated] - human	A;Gene: GDB:LPA
C;Species	Homo sapiens (man)	A;Cross-references: GDB:120699; OMIM:152200
C;Date:	30-Jun-1989 #sequence revision 30-Jun-1989 #text-change 08-Dec-2000	A;Map position: 6q26-6q27
C;Accession:	S00657; A28171; A47237; I60905; A47233; I55415; I55286	A;Note: several genes closely linked on chromosome 6 are identical in the first codon of kringle repeats
C;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fleiss, G.M.; Scan	C;Superfamily: apolipoprotein(a); kringle homology	
Nature 330, 132-137, 1987	C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; trypsin homology	
A;Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.	F;1-19/Domain: signal domain; #status predicted <SIG>	
A;Reference number: S00657; MUID:88039109	C;Genetics:	
A;Accession: S00657	A;Accession: 162867	
A;Molecule type: mRNA	A;Molecule type: DNA	
A;Residues: 1-14548 <MCU>	A;Residues: 1-16 <REB>	
A;Cross-references: GB:X06280; EMBL:306696; NID:928619; PIDN:CAA29618.1; PID:928620	A;Cross-references: GB:M90078; NID:9178786; PIDN:AAA35547.1; PID:9553188	
R;Eaton, D.L.; Fleiss, G.M.; Kahr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.	A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipoprotein(a) gene	
PROC: Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987	A;Accession: 16096	
A;Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to	A;Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ	
A;Reference number: A28017; MUID:87204109	A;Molecule type: DNA	
A;Accession: A28017	A;Accession: 162867	
A;Molecule type: protein	A;Accession: 162867	
A;Residues: 20-21, 'P', 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200-292-314, 'W', 316-31	A;Accession: 162867	
X, '4396-4401 <REB>	A;Accession: 162867	
R;Wade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meer, R.; Schwartz, R.	A;Accession: 162867	
PROC: Natl. Acad. Sci. U.S.A. 90, 1365-1373, 1993	A;Accession: 162867	
A;Title: 5' control regions of the apolipoprotein(a) gene and members of the related pl-	A;Accession: 162867	
A;Reference number: A47277; MUID:93165698	A;Accession: 162867	
A;Accession: A47277	A;Accession: 162867	
A;Status: preliminary; translation not shown; translated from GB/EMBL/DDBJ	A;Accession: 162867	
A;Molecule type: DNA	A;Accession: 162867	
A;Residues: 1-16 <REB>	A;Accession: 162867	
A;Cross-references: GB:I-07899; NID:967973; PID:9967974	A;Accession: 162867	
R;Malgaretti, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacch	A;Accession: 162867	

Query Match 29.4%; Score 1212.5; DB 1; Length 4548;
 Best Local Similarity 37.5%; Pred. No. 1.4e-76; Mismatches 251; Indels 93; Gaps 12;
 Matches 252; Conservative 76; Mismatches 251; Indels 93; Gaps 12;

QY 120 ENKDYIRNCILIGKRSYKTVSITKSGIKQPAHSMIPEHSELPPSYRGKDLOENYCNR 179
 Db 3888 ENSTGVODCYRGDCOSYRGLTSTTITGRTCOSWSMSMTPWHRRIPYVNAGLTRNYCRN 3947

QY 180 PRGEDEGGPWCFTSMEPVREVCVDIFQCSEVE----- 210
 Db 3948 PDAEI-RPKCYTMDPSVRKEYCINTRCPTVTESSLLTPWAVPVSTEAPSEQARPEKSPV 4006

QY 211 ---CMTCNCGESYRGLRDHRMHDGESKGICQRMPHQTPTRHKFLPERVDKGFDDNYCRNPDSGP 267
 Db 4007 VDQCYHGDGRSYRGISSTTWTGRCQSWSMSMTPWHRRIPENYPNAGLTENYCRNPDSK 4066

QY 268 RPWYTYLDHTRMAYCAIKTCADTM----NDTUVPLETE-----C10 307
 Db 4067 OPWCVYTTDPVCVRWBYCNLTOSETESGVLETPVTPVPUVPSMEAHSBAAPIBTQPTVVRQCYH 4126

QY 308 GOGEGIGRGVNTINGIPCQRWDSSQYPHEDMTEFNFCKDLRENCRPGDGSSPWCET 367
 Db 4127 GNGOSYRGCFSTTGTGRCQSWSMSMTPHRTQHNTYRPNGLNYCRPDGPGWCET 4186

QY 368 TDPNTRVGC-----QIPNCDMSHQDCYRGNKNMGNISQTRSG 409
 Db 4187 MDPSPIRWEYCNLTCSDTBTGVWVAPPVLOVPSLGPPSODCMGNGKORYRKATTIVG 4246

QY 410 LTCCKWPKDNEDLRHIFNEPDASK---INENYRNPPDDAHHGWCYTNPLIWDCPI 465
 Db 4247 TPCCEW--AAQEPHRHSTFTPGTKWAGLERKNYCRNPDPGDINGPWCYTMNPRKLFIDYCI 4304

QY 467 SRCGGDTTPITVNDHPVSCAKTKOLRVNGCIPTRNTGMMVSURYR-NKHIGGSLIK 525
 Db 4305 PLCCASS---FDGCKPQEPKKPGSIYGGCVAPHSNPWQVSLTRGKHFEGOTLIS 4360

QY 526 ESWWLTAROCFS-PSRDLKOEAWLGIDHVFGRGDKCKQVLNSOLVYPEGSLVLMKL 584
 Db 4361 PEWLTAAHCLKKSSRPSSYKVIGAHQEVLN-ESHVOEIEVSRLFETOQIAFLKL 4418

QY 585 ARPAPVLDVFSTIDLPNYGCTIPEKTSCSVYGGW3YGLTNYDGJLURV AHLYIMNEKCSQ 644
 Db 4419 SRPAVITDKVMPACLPSPDYMTARTECTITGWGETQTFGTGLIKEAQOLVIVENVCNH 4478

QY 645 HHRGKVTLNESEIAGAEGAIGKSGCGEGDGGPLCEOHKRMVYGGVIVPGRGAIPNRPG 704
 Db 4479 Y-----KYCAEHLARGTDSCQGDSSGGLVCFEKDVKYLQCVTSWNLGCRPNPKG 4529

QY 705 IFVRYAYAKWI 716
 Db 4530 VYARVSRVWVI 4541

GenCore version 4.5
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OM protein - protein search, using sw model

Run on : June 18, 2002, 17:46:19 ; Search time 13.55 Seconds
(without alignments)
2080.283 Million cell updates/sec

Title: US-09-423-516-2
Perfect score: 4125

Sequence: 1 MRWTKLILPALLQHVLHL.....VAYYAKWIKHKLITYKVYPOS 728

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

All number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	4126	100.0	728	1	HGF_HUMAN
2	3804	92.2	728	1	HGF_MOUSE
3	3802	92.1	728	1	HGF_RAT
4	1652	40.0	711	1	HGFEL_HUMAN
5	1602	38.8	716	1	HGFL_MOUSE
6	1446.5	35.1	790	1	PLMN_PIG
7	1408.5	34.1	812	1	PLMN_BOVIN
8	1379.5	33.4	812	1	PLMN_MOUSE
9	1370	33.2	810	1	PLMN_HUMAN
10	1369	33.2	810	1	PLMN_MACMO
11	1353.5	32.8	810	1	PLMN_ERTEU
12	1321.5	29.4	4548	1	APOA_HUMAN
13	1188.5	28.8	1420	1	APOA_MACMO
14	1583	14.1	343	1	PLMN_SHEEP
15	559.5	13.6	559	1	TPA_RAT
16	552.5	13.4	338	1	PLMN_HORSE
17	551.5	13.4	559	1	TPA_MOUSE
18	548.5	13.3	333	1	PLMN_CAMEL
19	543	13.2	625	1	THRB_BOVIN
20	539.9	13.1	566	1	TPA_BOVIN
21	532.5	12.9	562	1	TPA_HUMAN
22	531.5	12.9	618	1	THRB_MOUSE
23	527.5	12.8	622	1	THRB_HUMAN
24	518	12.6	617	1	THRB RAT
25	510.5	12.4	603	1	FA12_CAVPO
26	497.5	12.1	653	1	HGFA_MOUSE
27	480.5	11.6	655	1	HGFA_HUMAN
28	449	10.9	325	1	PLMN_PETRA
29	449	10.9	615	1	UROK_HUMAN
30	426.5	10.3	593	1	FA12_BOVIN
31	393	9.5	433	1	UROK_BOVIN
32	390	9.5	431	1	UROK_HUMAN
33	9.4		433	1	UROK_MOUSE

RESULT 1		ALIGNMENTS	
TD	HGF_HUMAN	STANDARD;	PRN; 728 AA.
AC	P14210; O9DUD6; Q9BYL9;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-AUG-1991 (Rel. 19, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Hepatocyte growth factor precursor (Scatter factor) (SF)		
DE	(Hepatopoietin A).		
DN	HGF OR HPTA.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX	NCBI_TAXID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	SEQUENCE FROM N.A.		
RC	TISSUE-Placenta;		
RX	MEDLINE-89332017; PubMed=2528952;		
RA	Miyazawa K., Tsubouchi H., Nakada D., Takahashi K., Okigaki M., Arakaki N., Nakayama H., Hiroto S., Sakiyama O., Takahashi K., Goida E., Daikuhara Y., Kitamura N.;		
RA	P26927 homo sapien		
RA	P26928 mus musculus		
RT	P06867 sus scrofa		
RT	P06868 bos taurus		
RL	P00747 homo sapien		
RP	P12545 macaca mulatta		
RP	P12545 erinaceus europaeus		
RP	P08519 homo sapien		
RA	P14417 macaca mulatta		
RA	P18654 ovis aries		
RP	P19637 rattus norvegicus		
RP	P80010 equus caballus		
RP	P11214 mus musculus		
RP	P80009 canis familiaris		
RP	P00735 bos taurus		
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RT	P12866 equus caballus		

very Match 92.2%; Score 3804; DB 1; Length 728;
Best Local Similarity 90.8%; Pred. No. 7.5e-277;
Matches 660; Conservative 39; Mismatches 26; Indels 2; Gaps 1;

1 MWVTKLKLPLQHVLHLUPLAITYAEGQRKRMVHEKKSAKTLLIDPAIKK 60
2 MNGTKLPLVLLQHVLLHLRHLVAPIAEGQRKRMVHEKKSAKTLLIDPAIKK 61

61 TRKVNTADOCANRCTRKGGLPPTCKAKAVFDKARRQCWPFNSMSSGVKEPGHEFDLYE 120
62 TRKVNSADECAHCRIRNGFTPKAVFEDKSRKCYWPENSMSSGVKKGGHEFDLYE 121

Db 121 NKDYIRNCITIGKGRSYKGTVSTTKSGRKQPNSSMIPHEHSFLPSSYRGKDLOEONYCRNP 180
122 NKDYIRNCIGKGGSYKGTVSTTKSGIKCQPNMSMIPHEHSFLPSSYRGKDLOEONYCRNP 181

181 RGEFGGPMCFTSNPEVRVCDFPQCSVECMTCNGSYRGJMDHTESGKTCORWDQTP 240
182 RGBEGGPWCFTSNPEVRVCDFPQCSVECMTCNGSYRGPMHDTESGKTCORWDQTP 241

Db 241 HRHKFLPERYPDKGFDNYCRNPDGKPERPWCVTLDPHTRWECAIKTCADNTMDTDYPL 300
Db 242 HRHKFLPERYPDKGFDNYCRNPDGKPERPWCVTLDPHTRWECAIKTCADNTMDTDYPL 301

Qy 301 EPTTCCIOQGEGYRGTVNTIWNQIPCQWDSQPMHEDMTPENFKCOLRENYCRNPDG 360
Db 362 EPTTCCIOQGEGYRGTVNTIWNQIPCQWDSQPMHEDMTPENFKCOLRENYCRNPDG 361

Qy 421 DLHRHIFEPDASKLNEWCRRPDDDAHGFWCYTGPNLPIWDYCPISRCEGDTPTIVNL 480
Db 422 DLHRHIFEPDASKLNEWCRRPDDDAHGFWCYTGPNLPIWDYCPISRCEGDTPTIVNL 481

Qy 481 DHFVVISCAKTLQRVNGIPTTRNIGWAVSLRVNRKHTCGGSILIKESEWLARQCFSR- 539
Qy 482 DHFVVISCAKTLQRVNGIPTTRNIGWAVSLRVNRKHTCGGSILIKESEWLARQCFSR- 541

Qy 540 -DLKDYEAWLGIHDVHGDEKCKQVKLNPOLVSVQYGPSCSDLVMLKRPALVDDFVSTD 598
Db 542 KDLKDYEAWLGIHDVHGDEKCKQVKLNPOLVSVQYGPSCSDLVMLKRPALVDDFVSTD 601

Qy 599 LPRYGCCTPEKUSSCVIGWGYIGLINVGLRVAHYIMGNEKCSQHKGKVNLNESEC 658
Db 602 LPSYGCCTPEKUSSCVIGWGYIGLINVGLRVAHYIMGNEKCSQHKGKVNLNESEC 661

Qy 659 AGAEKIGSGPCGEGDGGPLVCEOHKMRVLGVTPGRCAIPNRPGIFVRVAYAKWIK 718
Db 662 AGAEKIGSGPCGEGDGGPLVCEOHKMRVLGVTPGRCAIPNRPGIFVRVAYAKWIK 721

Qy 719 IILTYKV 725

Db 722 VILTYKL 728

RESULT 3

ID HGF_RAT
AC P17945;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
HGF.
OS Rattus norvegicus (Rat).
Oc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Ox NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=WISTAR; TISSUE=liver;
RX MEDLINE=90222197; Pubmed=2139229;
RA Toshiro K., Hagiya M., Nishizawa T., Seki T., Shimonishi M.,
RA Shinizu S., Nakamura T.;
RT "Reduced primary structure of rat hepatocyte growth factor and
expression of the mRNA in rat tissues.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
RN [2]
RC STRAIN=WISTAR; TISSUE=liver;
RX MEDLINE=91031482; Pubmed=2146117;
RA Okajima A., Miyazawa K., Kitamura N.;
CC "Primary structure of rat hepatocyte growth factor and induction of
its mRNA during liver regeneration following hepatic injury.";
CC EUR. J. Biochem. 193:375-381(1990).
CC RT IT HAS NO DETECTABLE PROTEASE ACTIVITY.
CC !- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL
HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPIC FACTOR, AND ACTS
AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES.
CC !- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
DISULFIDE BOND.
CC !- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
CC !- SIMILARITY: BELONGS TO PEPTIDE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
CC
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR D90102; BAA14133.1; -;
DR EMBL; X54400; CAA8266.1; -;
DR PIR; S13211; S13211.
DR PIR; A35644; A35644.
DR HSSP; P14210; BH1T.
DR MEROPS; S01.97.8; -;
DR InterPro; IPRO01314; Chymotrypsin.
DR InterPro; IPRO00001; Kringle.
DR InterPro; IPRO03014; PAN.
DR InterPro; IPRO03609; PanLAPP.
DR InterPro; IPRO01224; Trypsin.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRMTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR SMART; SM00120; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY_PSpec; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.

PRINTS; PRO001B; KRingle.	QY
SMART; SM00130; KR; 4.	DR
SMART; SM00473; PAN_AP; 1.	DR
SMART; SM00020; TYP_SPC; 1.	DR
PROSITE; PS00021; KRINGLE_1; 4.	DR
PROSITE; PS50070; KRINGLE_2; 4.	DR
PROSITE; PS50240; TRPSIN_DOM; 1.	DR
Kringle; Glycoprotein; Serine protease homolog; Signal;	POLYMORPHISM.
SIGNAL 1 18	POTENTIAL.
FT SIGNAL 19 711	HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
FT DOMAIN 32 109	PAR.
FT DOMAIN 110 186	KRINGLE 1.
FT DOMAIN 191 268	KRINGLE 2.
FT DOMAIN 283 361	KRINGLE 3.
FT DOMAIN 370 448	KRINGLE 4.
FT DISULFID 484 711	SERINE PROTEASE-LIKE.
FT DISULFID 506 78	BY SIMILARITY.
FT DISULFID 60 66	BY SIMILARITY.
FT DISULFID 110 186	BY SIMILARITY.
FT DISULFID 131 169	BY SIMILARITY.
FT DISULFID 157 181	BY SIMILARITY.
FT DISULFID 191 268	BY SIMILARITY.
FT DISULFID 194 324	INTERKRING (BY SIMILARITY).
FT DISULFID 212 251	BY SIMILARITY.
FT DISULFID 240 263	BY SIMILARITY.
FT DISULFID 283 361	BY SIMILARITY.
FT DISULFID 304 343	BY SIMILARITY.
FT DISULFID 332 355	BY SIMILARITY.
FT DISULFID 370 448	BY SIMILARITY.
FT DISULFID 391 431	BY SIMILARITY.
FT DISULFID 419 443	BY SIMILARITY.
FT DISULFID 468 588	INTERHAIN (BY SIMILARITY).
FT DISULFID 507 523	BY SIMILARITY.
FT DISULFID 602 667	BY SIMILARITY.
FT DISULFID 632 646	BY SIMILARITY.
FT DISULFID 657 685	BY SIMILARITY.
FT CARBOHYD 72 72	N-LINED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 296 296	N-LINED (GLCNAC . .) (POTENTIAL).
FT CARBOHYD 615 615	N-LINED (GLCNAC . .) (POTENTIAL).
FT VARIANT 13 13	Y -> C C -> F C -> P C -> F (IN REF. 2).
VARIANT 212 212	/FTID=VAR_006632.
FT CONFLICT 623 623	L -> F (IN REF. 2).
SEQUENCE 711 AA; 80379 MW; 596BD21F180290E4 CRC64; 5Q	Db 706 KVM 708
every Match 40.0%; Score 1652; DB 1; Length 711;	Db 706 KVM 708
Best Local Similarity 43.8%; Pred. No. 5. 2e-116;	Db 706 KVM 708
Matches 317; Conservative 103; Mismatches 265; Indels 38; Gaps 14;	Db 706 KVM 708
QY 16 LLHILLPLPAIIPAYAEGQRKRNTTHEFKKSAKTTLIKIDALKIK-TKVNTAQCANR 73	RESULT 5
QY 6 LLLILTOYLGVP--GO---RSPLNDFOVRLGTELQHLHLHAVVPGPWQEDVADAEBCAG 59	HGTL_MOUSE
QY 74 CTRNKGGLPPCTKAVFKDKARRQKCLQWFPNSMSGVKKEFGHEFDLJENKQVINGKIG 133	ID HGTL_MOUSE
QY 60 C---GPMDCRAPHYHNSSHGCQLPWQPHSPHLRGRGRCDFQKKYVRCIMNG 115	STANDARD;
QY 134 RSYKGTVSITKSGRKQCPNSMIPHEHSFLPSSYRGKQDLENYCRNPGRGEGGPWCFTSN 193	PRT; 716 AA.
QY 116 VGYRTMTATTVGGLFCQAWSHKFENDHKYPTPLRNG--LEENFCRNPDPGDPGGWCYTD 173	AC P26928;
QY 194 PEVRYEVCTIPOCEVECMNCNGESYRGLMDTESKGKIQQRWDHOPHRKFLPERYPD 253	DT 01-AUG-1992 (Rel. 23, Created)
QY 174 PAVRFQSCGKISCKREACYCWNCNGESYRGLMDTESKGKIQQRWDHOPHRKFLPERYPD 233	DT 01-AUG-1992 (Rel. 23, Last sequence update)
QY 254 GFDDNYCRNPDGQRPWCYTLDPHTRWENCAIKTCAADNTNNDTVPLETECIOQGEGY 313	DT 16-OCT-2001 (Rel. 40, Last annotation update)
QY 234 GLDDNYCRNPDGQRPWCYTLDPHTRWENCAIKTCAADNTNNDTVPLETECIOQGEGY 291	DE Hepatocyte growth factor-like protein precursor (Macrophage stimulatory protein) (MSP).
QY 718 KII 720	DE MSP1 OR HGFL.
RN [1]	GN Mus_musculus_(Mouse).
QO	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
QO	OX NCBI_TaxID:10090;
QO	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C; TISSUE=Liver;	RX MEDLINE=92002017; Published=1832957;
RA Friedzner Deegan S.J., Stuart L.A., Han S., Jamison C.S.;	RA
RT "Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor-like protein: expression during development.";	RT
RL Biochemistry 30:9781-9791(1991).	RL
CC -!- FUNCTION: PROBABLY NO PROTEOLYTIC ACTIVITY SINCE CRUCIAL AA	CC
CC CHARACTERISTIC OF SERINE PROTEASES CATALYTIC SITES ARE NOT	CC
CC -!- TISSUE SPECIFICITY: LIVER. LOWER LEVELS IN LUNG, PLACENTA AND	CC
CC ADRENAL.	CC
CC -!- DEVELOPMENTAL STAGE: IS EXPRESSED AT LOW LEVELS DURING GESTATION.	CC
CC JUST BEFORE BIRTH THE LEVEL INCREASES DRAMATICALLY AND REMAINS	CC
CC STABLE AFTERWARDS.	CC
CC -!- PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE POLYPEPTIDES.	CC
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between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC

OX NCBI_TaxID-9913;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RA Berglund L., Andersen M.D., Petersen T.E.;
 RT "Cloning and characterization of the bovine plasminogen cDNA";
 RL Int. Dairy J. 5;593-603(1995).
 RN [2] SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=85203906; PubMed=3846532;
 RA Schaller J., Moser P.W., Dannegger-Muller G.A.K., Rosselet S.J.,
 RA Kampfer U., Rickle E.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 human plasminogen.";
 RL Eur. J. Biochem. 149;267-278(1985).
 RN [3] SEQUENCE OF 706-812 FROM N.A.
 RX MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 human and bovine plasminogen.";
 RL Biochemistry 23;4243-4250(1984).
 RN [4] CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=81815329; PubMed=3356193;
 RA Marti T., Schaller J., Rickle E., Schmid K., Kammerling J.P.,
 RA Gerwig G.J., van Halbeek H., Villegenthart J.F.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 plasminogen. Species specificity in relation to sialylation and
 fucosylation patterns.";
 RL Eur. J. Biochem. 173;57-63(1988).
 CC -1- FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS
 A PROTEOLYTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING
 EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION,
 AND INFLAMMATION; IT WEAKENS THE WALLS OF THE
 GRAFTAFT FOLLICLE; IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN
 ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZYMOGENS, SUCH
 AS C1 AND C5. IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN,
 LAMININ AND VON WILLEBRAND FACTOR.
 CC -1- ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN
 ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO
 FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 CC -1- PTM: N-LINKED GLYCAN CONTAIN N-ACETYLGLUCOSAMINE AND SIALIC ACID.
 CC O-LINKED GLYCANS CONSIST OF GAL/GALNAc DISACCHARIDE WITH IS
 MODIFIED WITH UP TO 2 STERIC ACID RESIDUES (MICROHETEROGENEITY).
 CC -1- MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN
 IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.

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CC or send an email to license@isb-sib.ch)

CC EMBL; X79402; CAA35939.1; - .

DR EMBL; K02935; AAA30714.1; - .

DR PIR; A2591; PLOC.

DR HSSP; P00747; 2PK4.

DR MUROPS; S01_233; - .

DR Glycosuitedb; P06868; - .

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR00001; Kringle.

DR InterPro; IPR003014; PAN.

DR InterPro; IPR003609; Pan_apb.

DR InterPro; IPR001254; Trypsin.

DR Pfam; PF00051; kringle_5.

DR Pfam; PF00024; PAN_1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00018; KRINGLE.

DR SMART; SM00130; KR; 5.

DR SMART; SM00473; PAN_AP; 1.

DR PROSITE; PS0070; KRINGLE_2; 5.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SRP; 1.

KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;

KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Signal.

FT SIGNAL 1 26

FT CARBOHYD 365 365

FT CARBOHYD 365 365

FT CHAIN 27 812

FT CHAIN 27 812

FT CHAIN 584 812

FT DOMAIN 192 188

FT DOMAIN 192 188

FT DOMAIN 282 359

FT DOMAIN 384 461

FT DOMAIN 485 564

FT DOMAIN 584 812

FT CARBOHYD 315

FT CARBOHYD 315

FT ACT_SITE 624 624

FT ACT_SITE 667 667

FT ACT_SITE 762 762

FT CONFLICT 335 335

FT CONFLICT 516 516

FT CONFLICT 555 555

FT CONFLICT 744 744

FT SEQUENCE 812 AA; 91216 MN; 38A6A691E220946 CRC64;

Query Match 34.1%; Score 1408.5; DB 1; Length 812;

Best Local Similarity 35.4%; Pred. No. 9.6e-98; Indels 155; Gaps 15;

Matches 280; Conservative 117; Mismatches 240; Delins 155; Gaps 15;

QY 56 ALKKITKKVNTADOCANRCTRNRNKGPFCKAFVDFKARKQCQCLMPFNMSGGKKFGHE 115

Db 42 SLSRKKNLAGRSVDECAKC--EETEDFVCAFQYHSKQQCVVMAENSKNTPVFM-RD 97

QY 116 FDLYENKDVTRNCNLIGKGRSYKGIVSTKSGIKCOPWNSSMIPHEHSFLPSYSRKDQEN 175

Db 98 VILYEKRKYLLECKTGNGOTYRGTAETKGVICQWSATSPHPVKFSPEKEFPLAGLEEN 157

QY 176 YCRNPRLGEGPGFCFTSPVRYEVCDIPQCEVEMCWTGNGESYRGMIDHTESGKICRW 235

Db 158 YCRNPNDNGPWCYTDPDKYDCCP-EDKCMHCIGSNEGKIAKTMSGRDQAW 216

QY 236 DHQTPHRKFLPERVYDKGFFDDNCRNPDQGPQRPWCYTLDPHTRWECAIKTCAADNTMD 295

Db 217 DSQSPHAGYIPSKFPNKNMKMYCRNPDGEPPRCWFTDPQRWERCFCDIPRT---- 270

QY 296 TDVPLE-TTECIOGOGCGYRGTVNTINGIPOQRWDQSYPHEDHMTPEFKDLRENY 353

Db 271 TPPSSGPKYQCLKGTKGNIGGIVAVTESGHTCORMSEOTPHKHNRTPENFPCKNLEENY 330

QY 354 CRPDGSSPWCFTDPNTRVRGQCSQINCDMH-----GODCYGNG 396

Db 331 CRNPNERAKAPWCYTINSEWRWEYCT-IPSCESSPLSTERMDVPVPEOTPVDPCYHGNG 389

QY 397 KNYMGNLQSRTSGLTCMSW-----DKN----- 418

Db 390 OSYRGTSSTTGRKCOQWSMTPHRHLKTPENPNAGLTMNCRNPDADSKPWCYTFD 449

QY 419 ----- 418

Db 450 RVRNFCNLKCSETPEQVPAQGVENPPEADMIGTGSYRGKKATTAVGVPQEW 509

QY 419 -MEDLHRHIFWEPPDA--SKLNENYCRNPDDDAHGWPWCYTGNPLIPWDCYPISRCEDTT 474

RESULT 8
 PLMN_MOUSE STANDARD; PRT; 812 AA.
 ID PLMN_MOUSE
 P20918;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
 GN PLG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184812; PubMed=2081600;
 RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
 RT Characterization of the cDNA coding for mouse plasminogen and localization of the gene to mouse chromosome 17.ⁿ
 RL Genomics 8:49-61(1990).
 [2]
 RP CHARACTERIZATION OF ANGOSTATIN AND PARTIAL SEQUENCE.
 RX MEDLINE=95042728; PubMed=7525077;
 RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A., Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RL "Angiostatin, a novel angiogenesis inhibitor that mediates the suppression of metastases by a Lewis lung carcinoma." Cell 79:315-328(1994).
 -1 FUNCTION: PLASMIN DISSOLVES THE FIBRIN OF BLOOD CLOTS AND ACTS AS A PROTHROMBOTIC FACTOR IN A VARIETY OF OTHER PROCESSES INCLUDING EMBRYONIC DEVELOPMENT, TISSUE REMODELING, TUMOR INVASION, GRAFTANT FOLLICLE, IT ACTIVATES THE UROKINASE-TYPE PLASMINOGEN ACTIVATOR, COLLAGENASES AND SEVERAL COMPLEMENT ZIMOGENS, SUCH AS C1 AND C5, IT CLEAVES FIBRIN, FIBRONECTIN, THROMBOSPONDIN, LAMININ AND VON WILLEBRAND FACTOR.
 -1 FUNCTION: ANGIOSTATIN IS AN ANGIOGENESIS INHIBITOR THAT BLOCKS NEOVASCULARIZATION AND GROWTH OF EXPERIMENTAL PRIMARY AND METASTATIC TUMORS IN VIVO.
 -1 ENZYME REGULATION: CONVERTED INTO PLASMIN BY PLASMINOGEN ACTIVATORS, BOTH PLASMINOGEN AND ITS ACTIVATOR BEING BOUND TO FIBRIN. CANNOT BE ACTIVATED WITH STREPTOKINASE.
 -1 MISCELLANEOUS: PLASMIN IS INACTIVATED BY ALPHA-2-ANTIPLASMIN IMMEDIATELY AFTER DISSOCIATION FROM THE CLOT.
 -1 MISCELLANEOUS: IN THE PRESENCE OF THE INHIBITOR, THE ACTIVATION INVOLVES ONLY CLEAVAGE AFTER ARG-581, RESULTING IN 2 CHAINS HELD TOGETHER BY 2 DISULFIDE BONDS. WITHOUT THE INHIBITOR, THE ACTIVATION INVOLVES ALSO REMOVAL OF THE ACTIVATION PEPTIDE.
 -1 SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.

- [11] OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=82213905; PubMed=6919539;
RA TREXLER M., VALLI Z., PATTY L.;
RT "structure of the omega-aminocarboxylic acid-binding sites of human
plasminogen. Arginine 70 and aspartic acid 56 are essential for
binding of ligand by kringle 4";
RL J. Biol. Chem. 257:7401-7406(1982).
RN [12] FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS) OF 480-563.
RX MEDLINE=85054794; PubMed=6034526;
RA VALLI Z., PATTY L.;
RT "the fibrin-binding site of human plasminogen. Arginines 32 and 34
are essential for fibrin affinity of the kringle 1 domain";
RL J. Biol. Chem. 259:13690-13694(1984).
RN [13] PHOSPHORYLATION SITE SER-597.
RP MEDLINE=97345939; PubMed=9201958;
RA WANG H., PROCK M., BRETTHAUER R.K., CASTELLINO F.J.;
RT "Serine 578 is a major phosphorylation locus in human plasma
plasminogen";
RL Biochemistry 36:8100-8106(1997).
RN [14] CARBOHYDRATE-LINKAGE SITES.
RP MEDLINE=88155329; PubMed=3356193;
RA MARLI T., SCHALLER E.E., SCHMID K., KAMERLING J.P.,
RT "the N- and O-linked carbohydrate chains of human, bovine and porcine
plasminogen. Species specificity in relation to sialylation and
fucosylation patterns";
RL Eur. J. Biochem. 173:57-63(1988).
RN [15] CARBOHYDRATE-LINKAGE SITE 268.
RP MEDLINE=97207305; PubMed=9054441;
RA PARLE-SHEPHERD S.R., STEVENS R.D., ANDON N.L., ENGHILD J.J.,
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
human plasminogen 2";
RL J. Biol. Chem. 272:7408-7411(1997).
RN [16] CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RP MEDLINE=95042728; PubMed=7525077;
RA PIZZO S.V.;
RT "Angiotatin: a novel angiogenesis inhibitor that mediates the
suppression of metastases by a Lewis lung carcinoma";
RL Cell 79:315-328(1994).
RN [17] CHARACTERIZATION OF ANGIOSTATIN.
RP MEDLINE=97238710; PubMed=9102221;
RA SIM B.K., O'REILLY M.S., LIANG H., FORTIER A.H., HE W., MADSEN J.W.,
RT "A recombinant human angiostatin protein inhibits experimental primary
and metastatic cancer";
RL Cancer Res. 57:1329-1334(1997).
RN [18] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RP MEDLINE=92031352; PubMed=1657148;
RA MUJCHAK A.M., TULINSKY A., RAVICHANDRAN K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
refined at 1.9-A resolution";
RL Biochemistry 30:10576-10588(1991).
RN [19] X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RP MEDLINE=92031503; PubMed=1657149;
RA WU T.-P., PADMANABHAN K., TULINSKY A., MULICHAK A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
human plasminogen kringle 4";
RL Biochemistry 30:10589-10594(1991).
RN [20] X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RP STEC B., YAMAO R., WHITLOW M., TEETER M.M.;
RT Submitted (JUN-1995) to the PDB data bank.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM Protein - Protein search, using sw model
Run on : June 18, 2002, 17:45:54 ; Search time 34.17 Seconds
(without alignments)

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Title:

US-09-423-516-2

Perfect score:

4126

Score:

1

Sequence:

MWVTKILLPALLQHVLLHLL.....VAYYAKWIKHLILTYKVPOQ

728

Actual number of hits satisfying chosen parameters:

562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBML_19:
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_minc: *
8: sp_ooganelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_reptile: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT ID	PRELIMINARY;	PRT;	728 AA.
1	3880	94.0	728	6 QBBH09	QBBH09	QBBH09; PRELIMINARY;		
2	3170	76.8	726	13 Q90978		01-JUN-2001 (TREMBREL_17, Created)		
3	2806	68.0	710	13 Q91402		01-JUN-2001 (TREMBREL_17, Last sequence update)		
4	1704	41.3	716	13 Q91691		01-DEC-2001 (TREMBREL_19, Last annotation update)		
5	1652.5	40.1	717	13 P70006		HEPATOCYTE GROWTH FACTOR (HGF).		
6	1632	39.6	290	4 Q02935		OS Relis silvestris catus (Cat);		
7	1627	39.4	704	13 Q90865		OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
8	1624	39.4	296	4 Q14519		OC NCBI_TaxID:9685;		
9	1615	39.1	716	11 P70521		RN [1]		
10	1605	38.9	716	11 Q91XG8		RP TISSUE-LIVER; RA Kobayashi Y., Nakamura N., Ishizaka T., Masuda K., Ohno K., RA Tsujimoto H.,		
11	1579	38.3	709	13 Q90ZNG		RT "Molecular cloning of feline hepatocyte growth factor (HGF) cDNA,"		
12	1452	35.2	806	6 Q08783		RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases; CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE TRYPSIN FAMILY.		
13	1401.5	34.0	812	11 Q9R0W3		CC EMBL; AB046610; BAB21499.1; -.		
14	1398.5	33.7	812	11 Q91WJ5		DR HSSP; P14210; 1BAM.		
15	1371	33.2	810	4 Q15146		DR InterPro; IPR001314; Chymotrypsin.		
16	1365	33.1				DR InterPro; IPR00001; Kringle.		
						DR InterPro; IPR003014; PAN.		
						DR InterPro; IPR00609; Pan-asp.		
						DR InterPro; IPR00254; Trypsin.		
						DR Pfam; PF00051; Kringle; 1.		
						DR Pfam; PF00024; PAN; 1.		
						DR Pfam; PF0089; trypsin; 1.		
						DR Prints; PR00722; CHYMOTRYPSIN.		
						DR Prints; PR00018; KRINGLE.		
						DR SMART; SM01130; KR; 4.		
						DR SMART; SM00473; PAN_AP; 1.		
						DR SMART; SM00020; TRYSPC; 1.		
						DR PROSITE; PS00070; KRINGLE_1; UNKNOWN_4.		
						DR PROSITE; PS00070; KRINGLE_2; 4.		
						DR PROSITE; PS50240; TRYPSIN_DOM; 1.		

KW	Hydrolase; Serine protease.
SQ	SEQUENCE 728 AA; 83067 MW; 8D7F4A333D1E190A CRC64;
Query Match	94.0%; Score 3880; DB 6; Length 728;
Best Local Similarity	93.2%; Score 3880; DB 6; Length 728;
Matches	680; Conservative 28; Mismatches 18; Indels 4; Gaps 2;
Qy	1 MWTKLIPALLQHQVHLHLPLPIALPYAAGQRKRRTTHEFKSAKTLIDPALKIK 60
Db	1 MWTKLIPULLQHQVHLHLPLP...IPYAEQGKKRNLTHEFKSAKTLIDPALKIK 58
Oy	61 TKVNNTADOCANCRCTRNKGGLPTCKAFVFDKARQKOCCLWPPNNSMSSGVKKERGHEFDLYE 120
Db	59 TKMNPATQDCANCRCIRNKGLPFTCKAFEDKARKRCLWPENNTSGYKKERGHEFDLYE 118
Oy	121 NRDYRNCTIGKGRSYKGTWSITKSGIKCOPWSSMIPHEHSEFTPSSTRGKDQLENFCRNP 180
Db	119 NRDYRNCTIGKGRSYKGTWSITKSGIKCOPWSSMIPHEHSEFTPSSTRGKDQLENFCRNP 180
Oy	241 HRHFLPEXPYDGGDDWCNRDGPWRCPWCTLDPHTWRYCAIKTCADNTMDVPL 300
Db	239 HRHFLPERYPDGFDDNCRDPGKRPWCPYLTDTPWEPICAKMCAMSTMNDVPM 298
Oy	301 ETECIOQGEGRGTYNTIWNGIPQORWDSQYPHEHDMPENFKDKDIRENEYRNPDGS 360
Db	299 ETECIOQGEGRGTYNTIWNGIPQORWDSQYPHEHDMPENFKDKDIRENEYRNPDGS 360
Oy	361 ESPWCFTDPNIRVGTCSQPNCDMSHGQDCYRGNGKNTGNISOTRSGLTSMWDKNNM 420
Db	359 ESPWCFTDPNIRVGTCSQLPKCYQDSSQGQDCYRGNGKNTGNISOTRSGLTCSMWEKNNM 418
Oy	421 DHRHFWEPDAKSLNENYCRNPDDAHHGWCYGNPLPWDYKPISECEGDTPTVNL 480
Db	419 DLHRHFWEPDAKSLNENYCRNPDDAHHGWCYGNPLPWDYKPISECEGDTPTVNL 480
Oy	481 DHPVISACKQLQRLVNGIPTTRTIGWMWLSRYFRNKHCGGSILKESVWLTARQCFSSR- 539
Db	479 DHPVISACKQLQRLVNGIPTTRTIGWMWLSRYFRNKHCGGSILKESVWLTARQCFSSR- 539
Oy	540 -DLKOVEAWIGIHVGGRDEKCKQVLNSQLYVPGCSDVLMLKARPADVDFVSTD 598
Db	539 KDLKDEYAMLGIIHVHGRGDEKKRQVLNSQLYVPGCSDVLMLKARPADVDFVSTD 598
Oy	599 LPNGGCTIPEKTSQSVWYWGCGILINVDGLLVAHALYIMGNKCSOHRGKVLTNESEIC 658
Db	599 LPNGGCTIPEKTSQSVWYWGCGILINVDGLLVAHALYIMGNKCSOHRGKVLTNESEIC 658
Oy	659 AGBKIGSGPCESDYGAFLVCOHKMMVYLGTVPRGCAIPNRGIFVRYAVAYKWHK 718
Db	659 AGAINTVSGPCGEGDGGLPVLCEQHKMRVNLGVIVPRGCAIPNRGIFVRYAVAYKWHK 718
Oy	719 ILTYKIPQS 728
Db	719 ILTYKIPQS 728
RESULT	2
O90978	PRELIMINARY; PRT; 726 AA.
AC	Q90978; Q80866;
DT	01-JAN-1998 (REMBLLe. 05, Created)
DT	01-JAN-1998 (REMBLLe. 05, Last sequence update)
DT	01-DEC-2001 (REMBLLe. 19, Last annotation update)
DE	HEPATOCYTE GROWTH FACTOR / SCATTER FACTOR PRECURSOR.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
OX	NCBI_TAXID=9031;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-EMBRYO;
RX	MEDLINE=96039010; PubMed=755499;
RA	Thery C., Sharpe M.J., Barley S.J., Stern C.D., Gherardi E.;
RT	"Expression of HGF/SF, HGF/MS, and c-met suggests new functions during early chick development.", Dev. Genet. 17:90-101(1995).
RL	[2]
RN	SEQUENCE OF 1-409 FROM N.A.
RC	STRAIN=WHITE LEGHORN, AND RHODE ISLAND RED X LIGHT SUSSEX;
RX	TISSUE=EMBRYO; MEDLINE=95237013; PubMed=7720585;
RA	Streit A., Stein C.D., Thery C., Ireland G.W., Aparicio S., Sharpe M.J., Gherardi E.; Ireland G.W., Aparicio S.,
RT	"A role for HGF/SF in neural induction and its expression in Hensen's node during gastrulation.", Development 121:813-824(1995).
CC	-!- SIMILARITY: BILO3 TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
DR	EMBL; X84045; CAM58864.1; -;
DR	EMBL; X84045; CAM58864.1; -;
DR	EMBL; X84045; CAM56430.1; -;
DR	HSSP; P24120; BHPI.
DR	InterPro; IPR01114; Chymotrypsin.
DR	InterPro; IPR000001; Kringle.
DR	InterPro; IPR003014; PAN.
DR	InterPro; IPR002609; Pan.app.
DR	InterPro; IPR01254; Trypsin.
DR	Pfam; PF00051; Kringle_4.
DR	InterPro; IPR01114; Chymotrypsin.
DR	PRINTS; PRO0724; CHMOTRYSIN.
DR	SMART; SM00130; KR_4.
DR	SMART; SM00473; PAN_Ap_1.
DR	SMART; SM00020; TRYPSIN.
DR	PROSITE; PS00089; TRYPSIN.
DR	PROSITE; PS50070; KRINGLE_1.
DR	PROSITE; PS50070; KRINGLE_2.
DR	PROSITE; PS50070; KRINGLE_4.
DR	PROSITE; PS50340; TRYPSIN_DOMAIN.
KW	Alternative splicing; Glycoprotein; Growth factor; Hydrolase; Kringle; Serine protease; serine protease homolog; Signal; SIGNAL_CHAIN; SIGNAL_POTENTIAL.
FT	PT; CHAIN 28 726 AA; HEPATOCYTE GROWTH FACTOR/ SCATTER FACTOR.
SQ	SEQUENCE 726 AA; 82913 MW; 580510485766C38 CRC64;
Query Match	76.8%; Score 3170; DB 13; Length 726;
Best Local Similarity	74.5%; Pred. No. 1.4e-280;
Matches	544; Conservative 92; Mismatches 86; Indels 8; Gaps 3;
Qy	1 MWTKLIPALLQHQVHLHLPLPIALPYAAGQRKRRTTHEFKSAKTLIDPALKIK 60
Db	1 MWTKLIPULLQHQVHLHLPLP...IPYAEQGKKRNLTHEFKSAKTLIDPALKIK 58
Oy	61 TKVNNTADOCANCRCTRNKGGLPTCKAFVFDKARQKOCCLWPPNNSMSSGVKKERGHEFDLYE 120
Db	57 TKVNNTADOCANCRCTRNKGGLPTCKAFVFDKARQKOCCLWPPNNSMSSGVKKERGHEFDLYE 116
Oy	121 NRDYRNCTIGKGRSYKGTWSITKSGIKCOPWSSMIPHEHSEFTPSSTRGKDQLENFCRNP 180
Db	117 KKDYRNCTIGKGRSYKGTWSITKSGIKCOPWSSMIPHEHSEFTPSSTRGKDQLENFCRNP 180
Oy	181 RGEEGGPWCFTSNEPVYEVCDPQCSVECMCNGESYRGLMDHESGKICQRNDHQPL 240
Db	177 RGEEGGPWCFTSNEPVYEVCDPQCSVECMCNGESYRGLMDHESGKICQRNDHQPL 236
Oy	241 HRHFLPEXPYDGGDDWCNRDGPWRCPWCTLDPHTWRYCAIKTCADNTMDVPL 300
Db	237 HRHFLPERYPDGFDDNCRDPGKLRPWRCPYLDTPWEPFCAIKTCGVGJINSTEAVA 296
Oy	301 ETECIOQGEGRGTYNTIWNGIPQORWDSQYPHEHDMPENFKDKDIRENEYRNPDGS 360

Db	DR	PROSITE; PSS0240; TRYPSIN_DOM; 1.
OY	KW	Hydroxylase; Serine protease.
Db	SQ	SEQUENCE: 710 AA; 81487 MW; 5FE6480BE31C27FC CRC64;
QY	297	ETTCIQQGSGGRRGVNTIWSGICORWNQSOPHONITPPENFKCKDLDRENCRNPDGS 356
361	ESPWCFTDPNIRVGCGSOIPNCDSHGHGOLCQCYRGNGKMYNLTSRSGLTCMSMDKNAME 420	
357	ESPWCFTDPNIRKGCGSQIPKCDVSNEQDCYRGNGKSYGNLSKTRFGJTCSTWDKNIE 416	
421	DLRHRH-IFPFDASKLNEVNCRNDDDAHGWCYTGNPLIPWDYCPISEGDTPTIV 478	
417	DLRRHIOIFREPDKSLLKKNNCRNDDDFHGWCYTDDPLIPWDYCPISEGDTPTT 476	
Db	479	NLDHPVISCAKTKQLRVRVNGIPTPRNIGMVLWSYRNRKHICGGSLIKESWLTAROCFS 538
QY	: : : : : : : : : : : : : : :	
Db	477	SLDDVVIPCASTKHLRVNGISPTQNEGWTWSLTTRNKHICGGTLVKEEWTALAROCPFS 536
Db	478	IDLPWYCTIPEKTSVSYVWGYTGILINYQGLRVAHYLMNGNEKCSQHHRGKVLINESE 536
QY	R--DLKDYEAWLGTHDVHGRGDEKQVNLQNSOLVYGPESDSLVMKLARPAVLDFFVST 596	
Db	537	: : : : : : : : : : : : :
Db	539	RYKDLDKYKAWLGVHNINKGEEKHRQVRNTSOLIYGPACSDLVLLKSRPAILTNEF 596
Db	597	IRLPISGCTIPEKTSVSYVWGYTGILINYQGLRVAHYLMNGNEKCSQHHRGKVLINESE 556
Db	597	ICAGAEKIGSGPCEGDYGGPLVCEOKMRMLGVLYPGRCALIPNRPGFIVRVAYAKWI 716
QY	: : : : : : : : : : : : : :	
Db	657	ICAVAEITAGPCERDYGGPLVCEONRLKIVGVYIPGRGCAIRNRPGIFTFRVSYRSWI 716
Db	657	IPI- : : : : : : : : : : : :
QY	717 HKILRYKVP 726	
Db	717	: : : : : : : : : : : :
Db	717	HKIMMYRKp 726
RESULT	3	
091402	PRELIMINARY;	PRT; 710 AA.
091402	AC	091402; (TREMBrel. 01, created)
091402	DT	01-NOV-1996 (TREMBrel. 01, last sequence update)
091402	DT	01-NOV-1996 (TREMBrel. 19, Last annotation update)
091402	DE	HEPATOCYTE GROWTH FACTOR.
091402	GN	Xenopus.
091402	OS	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
091402	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
091402	OC	Xenopodinae.
091402	NCBI_TaxID	8333;
091402	RN	[1] SEQUENCE FROM N A.
091402	TISSUE	=TATLBUD;
091402	MEDLINE	-9267690; PubMed=7748783;
RA	RT	Nakamura H., Tashiro K., Nakamura T., shikawa K.;
RT	Xenopus early embryogenetics.; Mech. Dev. 49:123-131 (1995).	"Molecular cloning of xenopus HGF cDNA and its expression studies in Xenopus early embryogenetics.";
RL	CC	-1 SIMILARITY. BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRIPSIN FAMILY.
DR	EMBL; S77422; HSPB.	EMBL; S77410; IBHT.
DR	MEOPS; S01_976; -.	InterPro; IPR01314; Chymotrypsin.
DR	DR	InterPro; IPR00001; Kringle.
DR	DR	InterPro; IPR03014; PAN.
DR	DR	InterPro; IPR03609; Pan.app.
DR	DR	InterPro; IPR01254; Trypsin.
DR	DR	InterPro; IPR001314; Chymotrypsin.
DR	DR	PRINTS; PRO0018; KRINGLE.
DR	Pfam; PF00051; Kringle; 4.	PRINTS; PRO0024; PAN; 1.
DR	Pfam; PF00089; trypsin; 1.	PRINTS; PRO0072; CHMOTRTPSIN.
DR	PRINTS; PRO0018; KRINGLE.	PRINTS; PRO00130; KR; 4.
DR	SMART; SM00473; PAN_AP; 1.	SMART; SM00202; TRY_SP; 1.
DR	SMART; SM00021; KRINGLE; 3.	PROSITE; PS00021; KRINGLE; 3.
DR	PROSITE; PS55070; KRINGLE; 2; 4.	PROSITE; PS55070; KRINGLE; 2.
RESULT	4	
Q91691	PRELIMINARY;	PRT; 716 AA.
Q91691	ID	091691
Q91691	AC	091691;
Q91691	DT	01-NOV-1996 (TREMBrel. 01, last sequence update)
Q91691	DT	01-DEC-2001 (TREMBrel. 19, Last annotation update)
Q91691	DE	GROWTH FACTOR LIVERINE.
Q91691	OS	Xenopus laevis (African clawed frog).
Q91691	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Q91691	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Q91691	QY	HSPB; 719 HKILRYKVP 726
Q91691	Db	703 IMLYKAP 710

RX MEDLINE=97011125; PubMed=8958136;
RA Oshiro K., Iwama A., Matsuno R., Ezaki T., Sakamoto O., Hanaguchi I.,
RA Takasu N., Suda T.;
RT "Molecular cloning of Rat Macrophage-stimulating protein and its
involvement in the Male Reproductive System";
RT Biochem. Biophys. Res. Commun. 227:273-280(1996).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE
TRYPsin FAMILY.
EMBL: X95056; CAA64473.1; -.
DR HSSP; P00747; 1KRN.
DR MEROPS; S01.975; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro; IPR00001; Kringle.
DR InterPro; IPR00314; PAN.
DR InterPro; IPR003609; Pan app.
DR InterPro; IPR00125; Trypsin.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00089; trypsin; 1.
PRINTS; PRO00722; CHYMOTRYPSIN.
DR SMART; SMD0130; KR; 4.
DR SMART; SMD0473; PAN_AP; 1.
DR SMART; SMD0020; TRYP_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
KW Hydrolase; Serine protease; Signal.
FT SIGNAL 1 31 POTENTIAL.
SQ SEQUENCE 716 AA: 80733 MW: 068DF3E56D921F CRC64;

Query Match 39.1%; Score 1615; DB 11; Length 716;
Best Local Similarity 43.3%; Pred. No. 1.3e-138;
Matches 315; Conservative 118; Mismatches 254; Indels 40; Gaps 16;

QY 17 LHLILPIAIPIAEGOKRKRWTHEFKSAKTLIK-IDPAKIKTKK-VITADOCANR 74
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 4 LPILLILIAQCSRALGQ--RSPLNDPOLLRLTENLILHPPGPHQEDVADAECCR 60

QY 75 TRNKGLPFTCKAFVDFKARKOCLWFNSMSGVKKKEFGHEFDLYENKDVRNCITIGKR 134
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 ---GLLDCRAFHYNMSHCQQLWTHQSLRAQJHHSSLCDFQKDKDYRTCTIMNGA 116
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 135 SYKGTVSITKSGIKCOPWSMMPHENSHFLPSSYRKGDKLQENYCRAPIRGEEGGPWCFTSN 194
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 117 SYRTGTVARTADGLPCQAWSRREPNDHKYTPTPKNG--LEENFCRNPDPGDRPGPWCFTN 174
195 EVRYEVCDIPOCSEVCMTCNGESTYGLMHTESGKICORMDHQTPHRKELPERYPDKG 254
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 175 SVRFQSGIGKSCREAVCWMCNGEDYRGEVDTPEKPDG 234
QY 255 FDDNYCRNPDPGQPRCPWCYTLPDHTRMEYCAIKTCADN----TMNDTVPLETECI 307
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 235 LKDNYCRNPDASERPCKYTDPPNVEREFCDLPSCGNLLPPTKGSKSQRMKVKA 294
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 308 GOGEGRYRGTVNTIWINGIPCPQRDSQYPERHDMPENPKDLORENCRNPDPGSESPWCFT 367
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 295 GKGEDYRGTTNTISAGVCPQRCRNPDAQMPHQHFRVPEKTYACKDOLRENFCRNPDPGSEAWPCFT 354
368 TDPNIVGVCQIPNC-DMSIQDCYRGNKNYMGNIOSRGLCWSMKDNKMDLRHI 426
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 355 SRPGLRVAFCYQIPRCETEVVPEGCVHGSQVSKTRKGVOCQHW--SSETPHKPQ 412
QY 427 FWEPDA--SKLNENYCRNPDDAHCAGWCYGNPLPMDYCPISREGDTPTIVNDHPV 484
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 413 FTPTSAAPHAGIEANEFCRNPDPGDSERPCYTDPPNVEREFCDLPSCGNLLPPTVKGSKSQRMKVKA 293
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 307 QSGEGYRGTVNTIWINGIPCPQRDSQYPERHDMPENPKDLORENCRNPDPGSESPWCFT 366
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 294 RSKGEDYRGTTNTISAGVCPQRCRNPDAQMPHQHFRVPEKTYACKDOLRENFCRNPDPGSEAWPCFT 353
QY 367 TDPNIVGVCQIPNC-DMSIQDCYRGNKNYMGNIOSRGLCWSMKDNKMDLRHI 425
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 354 TSRPGLRVAFCYQIPRCETEVVPEGCVHGSQVSKTRKGVOCQHW--SSETPHKP 411
QY 426 TIWEPDASK--UNENFCRNPDDAHCAGWCYGNPLPMDYCPISREGDTPTIVNDHPV 483
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 412 QTPTSAFOAGIEANEFCRNPDPGDSERPCYTDPPNVEREFCDLPSCGNLLPPTVKGSKSQRMKVKA 471
QY 536 FPS--RDLKDYEAWLGIHDVHGRGDEKCKQVLYNVSQULVVGPEGSGSLVLMKLARPAYLD 593

RESULT 10
SQ 91XG8 ID Q91XG8 PRELIMINARY; PRT; 716 AA.
AC 091XG8; DT 01-DEC-2001 (Tremblel. 19' Created)
DT 01-DEC-2001 (Tremblel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblel. 19, Last annotation update)
DE HEPATOCYTE GROWTH FACTOR-LIKE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA Strausberg R.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL DR EMBL; BC010551; AAH10551.1; -.
SEQUENCE 716 AA: 12474C48A7D4B46D CRC64;

Query Match 38.9%; Score 1605; DB 11; Length 716;
Best Local Similarity 43.0%; Pred. No. 1.1e-17;
Matches 312; Conservative 113; Mismatches 203; Indels 38; Gaps 14;

QY 17 LHLILPIAIPIAEGOKRKRWTHEFKSAKTLIK--IDPAKIKTKKNTADOCANR 73
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 4 LPILLILIAQCSRALGQ--RSPLNDPOLLRLTENLILHPPGPHQEDVADAECCR 59
QY 74 CTRNKGKLPFTCKAFVDFKARKOCLWFNSMSGVKKKEFGHEFDLYENKDVRNCITIGK 133
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 60 C---GLLDCRAFHYNMSHCQQLWTHQSLRAQJHHSSLCDFQKDKDYRTCTIMNGA 115
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 134 RSYKGTVSITKSGIKCOPWSMMPHENSHFLPSSYRKGDKLQENYCRAPIRGEEGGPWCFTSN 193
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 116 VSYRTGTVARTAGLPCQAWSRREPNDHKYTPTPKNG--LEENFCRNPDPGDRPGPWCFTN 173
QY 194 EVRYEVCDIPOCSEVCMTCNGESTYGLMHTESGKICORMDHQTPHRKELPERYPDKG 253
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 174 RSVPFQSGIGKTCREAVCWMCNGEDYRGEVDTPEKPDG 233
QY 254 FDDNYCRNPDPGQPRCPWCYTLPDHTRMEYCAIKTCADN----IMNDTVPLETECI 306
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 234 DJKDNYCRNPDPGDSERPCYTDPPNVEREFCDLPSCGNLLPPTVKGSKSQRMKVKA 293
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 307 QSGEGYRGTVNTIWINGIPCPQRDSQYPERHDMPENPKDLORENCRNPDPGSESPWCFT 366
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 294 RSKGEDYRGTTNTISAGVCPQRCRNPDAQMPHQHFRVPEKTYACKDOLRENFCRNPDPGSEAWPCFT 353
QY 367 TDPNIVGVCQIPNC-DMSIQDCYRGNKNYMGNIOSRGLCWSMKDNKMDLRHI 425
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 354 TSRPGLRVAFCYQIPRCETEVVPEGCVHGSQVSKTRKGVOCQHW--SSETPHKP 411
QY 426 TIWEPDASK--UNENFCRNPDDAHCAGWCYGNPLPMDYCPISREGDTPTIVNDHPV 483
| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 412 QTPTSAFOAGIEANEFCRNPDPGDSERPCYTDPPNVEREFCDLPSCGNLLPPTVKGSKSQRMKVKA 471
QY 536 FPS--RDLKDYEAWLGIHDVHGRGDEKCKQVLYNVSQULVVGPEGSGSLVLMKLARPAYLD 593

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: June 18, 2002, 17:43:19 ; Search time 14.56 seconds

Perfect score: (without alignments)
US-09-423-516-2
4126

Sequence: 1 MWVTKLPLALLQHVLHL..... VAYYAKWIKKILTYKVQS 728

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents_AA:*
- 2: /cgn2_6/pctodata/2/iaa/5A_COMB.pep:*
- 3: /cgn2_6/pctodata/2/iaa/6A_COMB.pep:*
- 4: /cgn2_6/pctodata/2/iaa/6B_COMB.pep:*
- 5: /cgn2_6/pctodata/2/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/pctodata/2/iaa/backfiles1.pep:*

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4126	100.0	728	1 US-07-815-333A-2
2	4126	100.0	728	1 US-08-087-783A-22
3	4088.5	99.1	723	1 US-07-838-410-1
4	4088.5	99.1	723	1 US-08-290-937B-1
5	4088.5	99.1	723	1 US-08-444-641-1
6	4088.5	99.1	723	1 US-09-194-326-1
7	4085.5	99.0	723	1 US-08-290-937B-2
8	4079.5	98.9	723	1 US-08-290-937B-3
9	4077.5	98.8	723	4 US-08-030-410-3
10	4064.5	98.5	723	4 US-09-194-326-2
11	4064.5	98.5	723	4 US-09-194-326-3
12	3968	96.2	697	2 US-08-460-890A-50
13	3968	96.2	697	3 US-08-167-641C-50
14	3968	96.2	697	4 US-08-460-971A-50
15	3968	96.2	697	4 US-08-462-040-50
16	1654	40.1	711	2 US-08-766-982-2
17	1654	40.0	711	1 US-08-184-012C-8
18	1652	40.0	711	1 US-08-334-177-2
19	1652	40.0	711	2 US-08-296-219-2
20	1652	40.0	711	2 US-08-666-082B-1
21	1652	40.0	711	5 PCT-US95-13830-2
22	1608	39.0	716	2 US-08-766-982-1
23	1379.5	33.4	812	1 US-08-248-629A-1
24	1379.5	33.4	812	1 US-08-451-932-1
25	1379.5	33.4	812	1 US-08-452-260-1
27	1379.5	33.4	812	1 US-08-326-785-1

ALIGNMENTS

RESULT 1
US-07-815-333A-2
Sequence 2, Application US/07815333A
Patent No. 5342831

GENERAL INFORMATION:

APPLICANT: Nakamura, Toshikazu
TITLE OF INVENTION: EPITHELIOCYTE GROWTH ACCELERATOR

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Leydig, Voit & Mayer
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60601

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/815,333A
FILING DATE: 19911227
CLASSIFICATION: 5330

ATTORNEY/AGENT INFORMATION:

NAME: Green, Robert F.
REGISTRATION NUMBER: 27555
REFERENCE/DOCKET NUMBER: 44069

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 616-5500
TELEFAX: (312) 616-5700
TELEX: 25-3533

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein

US-07-815-333A-2

Query Match Score 100.0%; Score 4126; DB 1; Length 728;
Matches 728; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWVTKLPLALLQHVLHLPTAIPYEGQRKRNTTHEFKKSAKTTLIKDPALKIK 60
Db 1 MWVTKLPLALLQHVLHLPTAIPYEGQRKRNTTHEFKKSAKTTLIKDPALKIK 60

Patent No. 5200340

Qy	721	LTYKVPOQS	728
Db	721	LTYKVPOQS	728

OY	721	LTYKVPOS	728
Db	721	LTYKVPOS	728

OY	721	LTYKVPOS	728
Db	721	LTYKVPOS	728

OY	721	LTYKVPPOS	728
Db	721	LTYKVPPOS	728

OY	721	LTYKVPQS	728
Db	721	LTYKVPQS	728

OY	721	LTYKVPQS	728
Db	721	LTYKVPQS	728

QY 721 LTYKVPQS 728
Db 721 LTYKVPQS 728

NAME/KEY: ;
LOCATION: ;
OTHER INFO/RD: ;
OTHER INFO/RD: ;
US-07-838-410-1

OY 721 LTYKVPQS 728
Db 721 LTYKVPQS 728

SEARCHED: ; INDEXED: ; SERIALIZED: ; FILED: ;
LOCATION: 605.623 OTHER INFORMATION: /note= "IN
; OTHER INFORMATION: ; OTHER INFORMATION: ;
US-07-833-410-1

RESULT 3
 US-07-838-410-1
 Sequence 1, Application US/07838410
 Patent No. 5328836
GENERAL INFORMATION:
 APPLICANT: SHIMA, NOBUYUKI
 APPLICANT: HIGASHIO, KANJI
 APPLICANT: NAGAO, MASAYA
 APPLICANT: OGAKI, FUMIKO
 APPLICANT: TAKADA, HIROAKI
 APPLICANT: TSUDA, EIJI
 TITLE OF INVENTION: PLASMIDS CONTAINING DNA ENCODING THE AMINO ACID SEQUENCE OF TCF-II, TRANSFORMED CELLS WITH THE PLASMIDS, AND PRODUCTION METHOD OF BIOLOGICALLY ACTIVE SUBSTANCE USING THE TRANSFORMED CELLS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
 STREET: 2200 CLARENDON BLVD.
 CITY: ALEXANDRIA
 STATE: VA
 COUNTRY: USA
 ZIP: 22201
COMPUTER READABLE FORM:
 COMPUTER TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/838,410
 FILING DATE: 1992-03-11
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/JP91/00942
 FILING DATE: 15-JUL-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: JP 185852-1990
 FILING DATE: 13-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: WHITE, JOHN L.
 REGISTRATION NUMBER: 17,746
 REFERENCE/DOCKET NUMBER: WAK 110
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEX: 64191
INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 CELL TYPE: Fibroblast
FEATURE:
 NAME/KEY: Domain
 LOCATION: 393...405
 OTHER INFORMATION: /note= "INTERNAL AMINO ACID SEQUENCE IN ALPHA-CHAIN"
FEATURE:
 NAME/KEY: Protein
 LOCATION: 490...505
 OTHER INFORMATION: /note= "N-TERMINAL AMINO ACID SEQUENCE OF BETA-CHAIN"
 OTHER INFORMATION: SEQUENCE OF BETA-CHAIN
RESULT 4
 US-08-290-937B-1
 Sequence 1, Application US/08290937B
 Patent No. 5648233
GENERAL INFORMATION:
 APPLICANT: YAMAGUCHI, KYOJI
 APPLICANT: SHIMA, NOBUYUKI
 APPLICANT: MURAKAMI, AKIHIKO
 APPLICANT: GOTO, MASAKI
LOCATION: Domain
LOCATION: 605...623
OTHER INFORMATION: /note= "INTERNAL AMINO ACID SEQUENCE IN BETA-CHAIN"
OTHER INFORMATION: SEQUENCE OF BETA-CHAIN
RESULT 5
 US-07-838-410-1
 Query Match 99.1%; Score 4088.5; DB 1; Length 723;
 Best Local Similarity 99.3%; Pred. No. 0; Mismatches 0; Indels 5; Gaps Matches 723; Conservative 0; Mismatches 0; Indels 5; Gaps
Qy 1 MWVTKLPLALLJOHVLHLPLAPIYAEQORKRRTIHEFKKSAKTTLKIDPALKIK 60
Db 1 MWVTKLPLALLJOHVLHLPLAPIYAEQORKRRTIHEFKKSAKTTLKIDPALKIK 60
Qy 61 TKKVNTADOCANCRCTRNKGKGLPTCKAFVFDKARKQCWPFNSMSSGVKEFGHEDLY 120
Db 61 TKKVNTADOCANCRCTRNKGKGLPTCKAFVFDKARKQCWPFNSMSSGVKEFGHEDLY 120
Qy 181 RGEEGGPACFESNPPEVYEDCIPDOPSEVECTNGESYRGLMDHTESGKICORWDHOTP 240
Db 176 RGEEGGPACFESNPPEVYEDCIPDOPSEVECTNGESYRGLMDHTESGKICORWDHOTP 235
Qy 241 HRHKFLPERYDKGFDNYCRNPDGQPRPWYTLDPTRWECAIKCADNMDTPVPL 300
Db 236 HRHKFLPERYDKGFDNYCRNPDGQPRPWYTLDPTRWECAIKCADNMDTPVPL 295
Qy 301 ETTEC1QOGQEGYRGTNTINNGIPCORWDSOYPHEADMTPENPKCKDLRENYCRRNPDGS 360
Db 296 ETTEC1QOGQEGYRGTNTINNGIPCORWDSOYPHEADMTPENPKCKDLRENYCRRNPDGS 355
Qy 361 ESPWCFCITDPNTRVGCSQIQPNCDMSHGQDCYRGNNGNYMGNIQSQTSGLTCSSMDKNE 420
Db 356 ESPWCFCITDPNTRVGCSQIQPNCDMSHGQDCYRGNNGNYMGNIQSQTSGLTCSSMDKNE 415
Qy 421 DLHRHFLEWPASKLNLNCYCRNPDGDDAHGPMCYTGPNLIPADYCPCISRCEGOPTPTVNL 480
Db 416 DLHRHFLEWPASKLNLNCYCRNPDGDDAHGPMCYTGPNLIPADYCPCISRCEGOPTPTVNL 475
Qy 481 DHPVISCAKTKLVRVNGIPTRNIGNWMSLRYNKHCIGGLIKESWVLTARQCFPSRD 540
Db 476 DHPVISCAKTKLVRVNGIPTRNIGNWMSLRYNKHCIGGLIKESWVLTARQCFPSRD 535
Qy 541 LKDYEAWLGIHDVHGRDDECKKQLVNLSQLVYGGPEGSDLVLMKLPRAVLDDEVSITDLP 600
Db 536 LKDYEAWLGIHDVHGRDDECKKQLVNLSQLVYGGPEGSDLVLMKLPRAVLDDEVSITDLP 595
Qy 601 NYGCCTPEKTSQSYVGMGTYGLINDEGLRVAHLYIMNGNEKSQSHRGKVTLJNESETCAG 660
Db 596 NYGCCTPEKTSQSYVGMGTYGLINDEGLRVAHLYIMNGNEKSQSHRGKVTLJNESETCAG 655
Qy 661 AEKIGSGPCEGDIYGGPLVCEQHKMRMVLGVTVPGRGCAIPNRPGIFRVVAYAKWIHKII 720
Db 656 AEKIGSGPCEGDIYGGPLVCEQHKMRMVLGVTVPGRGCAIPNRPGIFRVVAYAKWIHKII 715

Query Match 99.1%; Score 4088.5; DB 1; length 723;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 723; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 MWYTKLLPALLQHVLULLLPLTAIPAIYPAEGQRNTRNTHEFKSAKTLIKIDPALIK 60
 Db 61 TKKVNTADOCANRCTRNRKGKLPFCKAFYDFDKARKQCLWEPFNNSGGYKKEFGHEFDLYE 120
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Qy 121 NKDVRNCITIGKGSYKGTVSKSGIKQWPSSMIPREHSFLLESSYRKDKLOENYCRNP 180
 121 NKDVRNCITIGKGSYKGTVSKSGIKQWPSSMIPREHSFLLESSYRKDKLOENYCRNP 180

Db 181 RGEGGPWCFTSNNEVRYEVCDIPOCSEVECMTGNGESYRGLMDHTESGKICORNWDHOTP 240
 181 RGEGGPWCFTSNNEVRYEVCDIPOCSEVECMTGNGESYRGLMDHTESGKICORNWDHOTP 240

Db 176 RGSEGGPWCFTSNNEVREVCDFQCSVECMTCNGESYRGLMDHTESGKICORNWDHOTP 235
 241 HRHKFLPERYPDKGFDNYCRNPDQGQPRPCYTDLPHTRWEYCAIKCADNTMDTVP 300
 241 HRHKFLPERYPDKGFDNYCRNPDQGQPRPCYTDLPHTRWEYCAIKCADNTMDTVP 300

Qy 236 HRHKFLPERYPDKGFDNYCRNPDQGQPRPCYTDLPHTRWEYCAIKCADNTMDTVP 295
 301 ETTECIOQGEGFRGVNTIWIWTPCQRMDSQFPHEDMTPENPKDIRENCRNPDGS 360
 296 ETTECIOQGEGFRGVNTIWIWTPCQRMDSQFPHEDMTPENPKDIRENCRNPDGS 355

Qy 361 ESPWCFTDPNIRGYCQSOIPNCMDMSHGDCYRNGKNMGNLSQTREGSLTCMNDKME 420
 Db 356 ESPWCFTDPNIRGYCQSOIPNCMDMSHGDCYRNGKNMGNLSQTREGSLTCMNDKME 415

Qy 421 DLHRHFWEPPDASKLNENYCRRNPDDAHCAGPWCYTGNPLIPWDYCPISRCEGDTPTIVNL 480
 Db 416 DLHRHFWEPPDASKLNENYCRRNPDDAHCAGPWCYTGNPLIPWDYCPISRCEGDTPTIVNL 475

Qy 481 DHPIVISCAKKQLRVNGIPPTRTNIGWMVSLRVRKHNKGSLIKESAVLTAROCPFSRD 540
 Db 476 DHPIVISCAKKQLRVNGIPPTRTNIGWMVSLRVRKHNKGSLIKESAVLTAROCPFSRD 535

Qy 541 LKDYEAWLGHIDVYGRGDECKKQWLNVSOLWYPEGSDLVMKLARPALVDDRFSTIDLP 600
 Db 536 LKDYEAWLGHIDVHGRGDECKKQWLNVSOLWYPEGSDLVMKLARPALVDDRFSTIDLP 595

Qy 601 NYGCTIPEKTSCSVYGWGTYGLINYDGLRVAHYIMGNEKCSQHRSKVLTNESETCAG 660
 Db 596 NYGCTIPEKTSCSVYGWGTYGLINYDGLRVAHYIMGNEKCSQHRSKVLTNESETCAG 655

Qy 661 AEKIGSGPCEGDDYQGPLVCEQHMRMVLGVIVPORGCAIPNRPGIFVRVAYYKWHII 720
 Db 656 AEKIGSGPCEGDDYQGPLVCEQHMRMVLGVIVPORGCAIPNRPGIFVRVAYYKWHII 715

Qy 721 LTYKVPQS 728
 Db 716 LTYKVPQS 723

ATTORNEY/AGENT INFORMATION:
 NAME: CAMPBELL, PAULA A.
 REGISTRATION NUMBER: 32_503
 REFERENCE/DOCKET NUMBER: FJN-022
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 248-7000
 TELEFAX: (617) 248-7100
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-290-937B-1

RESULT 5
 US-08-404_643-1
 ; Sequence 1, Application US/08404643
 ; Patent No. 5658742
 ; GENERAL INFORMATION:
 ; APPLICANT: HIGASHIO, KANJI
 ; APPLICANT: SHIMA, NOBUKRI
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODY
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
 ; STREET: 53 STATE STREET
 ; CITY: BOSTON
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patienten Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/404_643
 FILING DATE: 15-MAR-1995
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: CAMPBELL, PAULA A.
 REGISTRATION NUMBER: 32_503
 REFERENCE/DOCKET NUMBER: FJN-034 (3999/35)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)-248-7100
 TELEFAX: (617)-248-7100
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-404-643-1

Query Match 99.1%; Score 4088.5; DB 1; length 723;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 723; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

TOPLOGY: linear
; MOLECULE TYPE: protein
; US-08-290-937B-3

Query Match 98.9%; Score 4079.5; DB 1; Length 723;
; Best Local Similarity 99.0%; Pred. No. 0; Mismatches 1; Indels 5; Gaps 1;
; Matches 721; Conservative 1; Mismatches 1;

QY 1 MWYTKLPLALLQHVLHLILLIPIAIPIAEGOKRRNTHIEFKSAKTLIKIDPALKIK 60
; 1 MWYTKLPLALLQHVLHLILLIPIAIPIAEGOKRRNTHIEFKSAKTLIKIDPALKIK 60

QY 61 TRKVNTADOCANCTRNGKLGLPFCKATVFDKARKQC1WFPFNSMSSGVKKERGHEFOLYE 120
; 61 TRKVNTADOCANCTRNGKLGLPFCKATVFDKARKQC1WFPFNSMSSGVKKERGHEFOLYE 120

QY 121 NKDYIRNCITIGKGRSYKGTVSITKSGIKCOPNSMITHEHSPFLPSSTRGKDQIENYCNP 180
; 121 NKDYIRNCITIGKGRSYKGTVSITKSGIKCOPNSMITHEHSPFLPSSTRGKDQIENYCNP 180

QY 181 RGERGGPWCFTSNPEVRVCDIPQCSVECMTCNGESYRGLMDHTESGRICCRWDQTP 240
; 181 RGERGGPWCFTSNPEVRVCDIPQCSVECMTCNGESYRGLMDHTESGRICCRWDQTP 240

QY 176 RGERGGPWCFTSNPEVRVCDIPQCSVECMTCNGESYRGLMDHTESGRICCRWDQTP 235
; 176 RGERGGPWCFTSNPEVRVCDIPQCSVECMTCNGESYRGLMDHTESGRICCRWDQTP 235

QY 241 HRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 300
; 241 HRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 300

Db 236 HRRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 295
; 236 HRRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 295

QY 301 ETTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 360
; 301 ETTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 360

Db 296 ESTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 355
; 296 ESTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 355

Qy 361 ESPWCFTDPNIRVGYCSQIPNCMDMSHQCDCYRNGKNYMGNIQSOTRSGLTC5MWDKME 420
; 361 ESPWCFTDPNIRVGYCSQIPNCMDMSHQCDCYRNGKNYMGNIQSOTRSGLTC5MWDKME 420

Db 356 ESPWCFTDPNIRVGYCSQIPNCMDMSHQCDCYRNGKNYMGNIQSOTRSGLTC5MWDKME 415
; 356 ESPWCFTDPNIRVGYCSQIPNCMDMSHQCDCYRNGKNYMGNIQSOTRSGLTC5MWDKME 415

QY 421 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 480
; 421 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 480

Db 416 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 475
; 416 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 475

QY 481 DHVVISCAKTKOLRVVNGIPTTRNIGMWSLRYRKHKGSLIKESWLTARQCFPSRD 540
; 481 DHVVISCAKTKOLRVVNGIPTTRNIGMWSLRYRKHKGSLIKESWLTARQCFPSRD 540

Db 476 DHVVISCAKTKOLRVVNGIPTTRNIGMWSLRYRKHKGSLIKESWLTARQCFPSRD 535
; 476 DHVVISCAKTKOLRVVNGIPTTRNIGMWSLRYRKHKGSLIKESWLTARQCFPSRD 535

QY 541 LKDYEAMLGIHUVHGRDECKOVLNTSOLVYGGPEGSDLVIMKLARPAVLDFFSTIDLP 600
; 541 LKDYEAMLGIHUVHGRDECKOVLNTSOLVYGGPEGSDLVIMKLARPAVLDFFSTIDLP 600

Db 536 LKDYEAMLGIHUVHGRDECKOVLNTSOLVYGGPEGSDLVIMKLARPAVLDFFSTIDLP 595
; 536 LKDYEAMLGIHUVHGRDECKOVLNTSOLVYGGPEGSDLVIMKLARPAVLDFFSTIDLP 595

QY 601 NYGCTIPEKTSQSVYGMQTYGLINQDGLRVALHLIYKNGNEKCSQOHRCVKVLINESEICAG 660
; 601 NYGCTIPEKTSQSVYGMQTYGLINQDGLRVALHLIYKNGNEKCSQOHRCVKVLINESEICAG 660

Db 596 NYGCTIPEKTSQSVYGMQTYGLINQDGLRVALHLIYKNGNEKCSQOHRCVKVLINESEICAG 655
; 596 NYGCTIPEKTSQSVYGMQTYGLINQDGLRVALHLIYKNGNEKCSQOHRCVKVLINESEICAG 655

QY 661 AEKIGSGCGCEGYGGPLVCEQHMKRMVILGVITVPGRGCAIPNRPQIFVRYVAYAKWIHKII 720
; 661 AEKIGSGCGCEGYGGPLVCEQHMKRMVILGVITVPGRGCAIPNRPQIFVRYVAYAKWIHKII 720

Db 656 AEKIGSGCGCEGYGGPLVCEQHMKRMVILGVITVPGRGCAIPNRPQIFVRYVAYAKWIHKII 715
; 656 AEKIGSGCGCEGYGGPLVCEQHMKRMVILGVITVPGRGCAIPNRPQIFVRYVAYAKWIHKII 715

QY 721 LTYKVPQS 728
; 721 LTYKVPQS 728

Db 716 LTYKVPQS 723
; 716 LTYKVPQS 723

RESULT 9
; US-08-030-410-3
; Sequence 3, Application us/08030410
; Patent No. 6223359

GENERAL INFORMATION:
; APPLICANT: Komiyama, Atsushi
; APPLICANT: Nakahata, Tatsutoshi
; APPLICANT: Kubo, Tetsuo
; APPLICANT: Tanaka, Ryuei
; APPLICANT: Kawano, Genji
; APPLICANT: Sudo, Tetsuo

APPLICANT: Sano, Emiko
; APPLICANT: Kojima, Katsuaki
; TITLE OF INVENTION: HEMOPOETIC STEM CELL MULTIPLIER
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08030.410
; FILING DATE: 19930521
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGI-LO, Frank S.
; REGISTRATION NUMBER: 31,346
; APPLICATION/ROCKET NUMBER: 8898

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 723 amino acids
; LENGTH: 723 amino acids
; TYPE: amino acid
; TOPLOGY: linear
; MOLECULE TYPE: protein
; US-08-030-410-3

Query Match 98.8%; Score 4077.5; DB 4; Length 723;
; Best Local Similarity 98.9%; Pred. No. 0; Mismatches 2; Indels 5; Gaps 1;
; Matches 720; Conservative 2; Mismatches 1; Indels 5; Gaps 1;

QY 1 MWYTKLPLALLQHVLHLILLIPIAIPIAEGOKRRNTHIEFKSAKTLIKIDPALKIK 60
; 1 MWYTKLPLALLQHVLHLILLIPIAIPIAEGOKRRNTHIEFKSAKTLIKIDPALKIK 60

QY 121 NKDYIRNCITIGKGRSYKGTVSITKSGIKCOPNSMITHEHSPFLPSSTRGKDQIENYCNP 180
; 121 NKDYIRNCITIGKGRSYKGTVSITKSGIKCOPNSMITHEHSPFLPSSTRGKDQIENYCNP 180

QY 181 RGERGGPWCFTSNPEVRVCDIPQCSVECMTCNGESYRGLMDHTESGRICCRWDQTP 240
; 181 RGERGGPWCFTSNPEVRVCDIPQCSVECMTCNGESYRGLMDHTESGRICCRWDQTP 240

QY 241 HRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 300
; 241 HRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 300

Db 236 HRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 295
; 236 HRHKFLPERYPDKGFDNYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 295

QY 301 ETTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 360
; 301 ETTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 360

Db 296 ETTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 355
; 296 ETTEC1OQCGEGYRGTVNTIWINGIPCQWDSQPHEDHMTPENPKCHDLRENYCNP 355

QY 361 ESPWCFTDPNIRVGYCSQIPNCMDMSHQCDCYRNGKNYMGNIQSOTRSGLTC5MWDKME 420
; 361 ESPWCFTDPNIRVGYCSQIPNCMDMSHQCDCYRNGKNYMGNIQSOTRSGLTC5MWDKME 420

Db 421 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 480
; 421 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 480

Db 416 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 475
; 416 DLHRHFWEPDASKLNENYCRNPDGQPRWCYTLDPHTRWEXCAIKTCADNTMDTVP 475

QY 481 DHPVISCAKTKOLRVNGIPTRNIGWMSLRYRNKHICGGSLIKESWLTAQCPFSDR 540
 Db 536 LKDYEAWLGJHDVHGRGDECKQVLNVSQLVYGPESDSLVMKLARPALVDDFVSTIDLP 595
 QY 601 NYGCTIPEKTSCSVYWGWTGLINYDGLLRLVAHYLIMGNNEKCSOHRKGVTLNESICAG 660
 Db 596 NYGCTIPEKTSCSVYWGWTGLINYDGLLRLVAHYLIMGNNEKCSOHRKGVTLNESICAG 655
 QY 661 AEKIGSGPCEGDDGGPLVCEQHKMRMVGIVPREGCAIPNRPIFVRVAYAKWHKII 720
 Db 656 AEKIGSGPCEGDDGGPLVCEQHKMRMVGIVPREGCAIPNRPIFVRVAYAKWHKII 715
 QY 721 LTYKVPOS 728
 Db 716 LTYKVPOS 723

RESULT 10
 US-09-194-326-2
 ; Sequence 2, Application US/09194326
 ; Patent No. 6306827
 ; GENERAL INFORMATION:
 ; APPLICANT: Kinosaki, Masahiko
 ; APPLICANT: Ogawa, Hiroki
 ; APPLICANT: Masanaga, Hiroaki
 ; APPLICANT: Kobayashi, Fumie
 ; APPLICANT: Yamaguchi, Kyoji
 ; TITLE OF INVENTION: Agent for Preventing and/or Treating Renal Disease
 ; FILE REFERENCE: FJN-069
 ; CURRENT APPLICATION NUMBER: US/09/194,326
 ; CURRENT FILING DATE: 1998-11-24
 ; EARLIER APPLICATION NUMBER: PCT/JP98/01221
 ; EARLIER FILING DATE: 1998-03-20
 ; EARLIER APPLICATION NUMBER: JP 94989
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO: 2
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: RKRRAAAA
 ; OTHER INFORMATION: mutant of TCF-II
 ; OTHER INFORMATION: 09-194-326-2

Query Match 98.5%; Score 4064.5; DB 4; Length 723;
 Best Local Similarity 98.8%; Pred. No. 0; Mismatches 4; Indels 5; Gaps 1;
 Matches 719; Conservative 0; MisMatches 4; Indels 5; Gaps 1;

QY 1 MWVTKLPLALLQHVLLHLLPLPAIPYAEGRKRRNTTHEFKSAKTLIKIDPALIK 60
 Db 1 MWVTKLPLALLQHVLLHLLPLPAIPYAEGRKRRNTTHEFKSAKTLIKIDPALIK 60

QY 61 TKKVWADCANRCTRNKGKLFPTCKAFVDFDKARKOCLWFPTNSMSGVKEFGHEFDLYE 120
 Db 61 TKKVWADCANRCTRNKGKLFPTCKAFVDFDKARKOCLWFPTNSMSGVKEFGHEFDLYE 120

QY - 121 NKDYRNCTTGKGRSKYKGWTGKPSMIPHEISFLPLSSYRGKQLOQENICRNP 180
 Db 121 NKDYRNCTTGKGRSKYKGWTGKPSMIPHEISFLPLSSYRGKQLOQENICRNP 180

Db 121 NKDYRNCTTGKGRSKYKGWTGKPSMIPHEISFLPLSSYRGKQLOQENICRNP 175

QY 181 RGEEGGPWCTTSNPEVRECVCDIPOCSEVECMTNGCESYRGLMDHTESGKICQRMHQTP 240
 Db 176 RGEEGGPWCTTSNPEVRECVCDIPOCSEVECMTNGCESYRGLMDHTESGKICQRMHQTP 235

QY 241 HRKELPERPDKGFDDNYCENPDGOPRPMCYLDPHTRWRYCAIKTCADNTMNDTDPVPL 300

RESULT 11
 US-09-194-326-3
 ; Sequence 3, Application US/09194326
 ; Patent No. 6306827
 ; GENERAL INFORMATION:
 ; APPLICANT: Kinosaki, Masahiko
 ; APPLICANT: Ogawa, Hiroki
 ; APPLICANT: Masanaga, Hiroaki
 ; APPLICANT: Kobayashi, Fumie
 ; APPLICANT: Yamaguchi, Kyoji
 ; APPLICANT: Higashio, Kanji
 ; TITLE OF INVENTION: Agent for Preventing and/or Treating Renal Disease
 ; FILE REFERENCE: FJN-069
 ; CURRENT APPLICATION NUMBER: US/09/194,326
 ; CURRENT FILING DATE: 1998-11-24
 ; EARLIER APPLICATION NUMBER: PCT/JP98/01221
 ; EARLIER FILING DATE: 1998-03-20
 ; EARLIER APPLICATION NUMBER: JP 94989
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO: 3
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: RKRRAAAA
 ; OTHER INFORMATION: mutant of TCF-II
 ; OTHER INFORMATION: 09-194-326-3

Query Match 98.5%; Score 4064.5; DB 4; Length 723;
 Best Local Similarity 98.8%; Pred. No. 0; Mismatches 4; Indels 5; Gaps 1;
 Matches 719; Conservative 0; MisMatches 4; Indels 5; Gaps 1;

QY 1 MWVTKLPLALLQHVLLHLLPLPAIPYAEGRKRRNTTHEFKSAKTLIKIDPALIK 60
 Db 1 MWVTKLPLALLQHVLLHLLPLPAIPYAEGRKRRNTTHEFKSAKTLIKIDPALIK 60

QY 61 TKKVWADCANRCTRNKGKLFPTCKAFVDFDKARKOCLWFPTNSMSGVKEFGHEFDLYE 120
 Db 61 TKKVWADCANRCTRNKGKLFPTCKAFVDFDKARKOCLWFPTNSMSGVKEFGHEFDLYE 120

QY - 121 NKDYRNCTTGKGRSKYKGWTGKPSMIPHEISFLPLSSYRGKQLOQENICRNP 180
 Db 121 NKDYRNCTTGKGRSKYKGWTGKPSMIPHEISFLPLSSYRGKQLOQENICRNP 180

Db 121 NKDYRNCTTGKGRSKYKGWTGKPSMIPHEISFLPLSSYRGKQLOQENICRNP 175

QY 181 RGEEGGPWCTTSNPEVRECVCDIPOCSEVECMTNGCESYRGLMDHTESGKICQRMHQTP 240
 Db 176 RGEEGGPWCTTSNPEVRECVCDIPOCSEVECMTNGCESYRGLMDHTESGKICQRMHQTP 235

QY 241 HRKELPERPDKGFDDNYCENPDGOPRPMCYLDPHTRWRYCAIKTCADNTMNDTDPVPL 300

RESULT 12
 US-09-194-326-4
 ; Sequence 4, Application US/09194326
 ; Patent No. 6306827
 ; GENERAL INFORMATION:
 ; APPLICANT: Kinosaki, Masahiko
 ; APPLICANT: Ogawa, Hiroki
 ; APPLICANT: Masanaga, Hiroaki
 ; APPLICANT: Kobayashi, Fumie
 ; APPLICANT: Yamaguchi, Kyoji
 ; APPLICANT: Higashio, Kanji
 ; TITLE OF INVENTION: Agent for Preventing and/or Treating Renal Disease
 ; FILE REFERENCE: FJN-069
 ; CURRENT APPLICATION NUMBER: US/09/194,326
 ; CURRENT FILING DATE: 1998-11-24
 ; EARLIER APPLICATION NUMBER: PCT/JP98/01221
 ; EARLIER FILING DATE: 1998-03-20
 ; EARLIER APPLICATION NUMBER: JP 94989
 ; NUMBER OF SEQ ID NOS: 3
 ; SEQ ID NO: 3
 ; LENGTH: 723
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: KIKKKK27A1ATA
 ; OTHER INFORMATION: mutant of TCF-II
 ; OTHER INFORMATION: 09-194-326-3

Query Match 98.5%; Score 4064.5; DB 4; Length 723;
 Best Local Similarity 98.8%; Pred. No. 0; Mismatches 4; Indels 5; Gaps 1;
 Matches 719; Conservative 0; MisMatches 4; Indels 5; Gaps 1;

QY 1 MWVTKLPLALLQHVLLHLLPLPAIPYAEGRKRRNTTHEFKSAKTLIKIDPALIK 60

MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FASTSEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,890A
 FILING DATE: June 5, 1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/167,641
 FILING DATE: December 14, 1993
 APPLICATION NUMBER: 07/855,389
 FILING DATE: March 20, 1993
 APPLICATION NUMBER: PCV/US/3/02725
 FILING DATE: March 19, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 222/066
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 697 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US - 08-460-890A-50

Query Match 96.2%; Score 3968; DB 2; Length 697;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 697; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 ORKRKNTIHERPKSKAKTTLKIDPAALKIKRKVNTRADQANCRCTRNKGKLPFTCKAFVFDK 91
 Db 1 QRKRKNTIHERPKSKAKTTLKIDPAALKIKRKVNTRADQANCRCTRNKGKLPFTCKAFVFDK 60

QY 92 ARKQOLWPNMSMSGVKKEFGEHDLYENKYDNYIRNCITGGRSYKGTVSITSKSIKQCP 151
 Db 61 ARKQOLWPNMSMSGVKKEFGEHDLYENKYDNYIRNCITGGRSYKGTVSITSKSIKQCP 120

QY 152 WSSMPHESFLPNSMSSGGVKKBERGFEDLYENKYDNYIRNCITGGRSYKGTVSITSKSIKQCP 211
 Db 121 WSSMPHESFLPNSMSSGGVKKBERGFEDLYENKYDNYIRNCITGGRSYKGTVSITSKSIKQCP 180

QY 212 MTCNGNOSRSYRGLMDHTESGKICQRWHQTPIRHKFEPERYPDKGFDNNYCRNPDDGQPRWC 271
 Db 181 MTCNGNOSRSYRGLMDHTESGKICQRWHQTPIRHKFEPERYPDKGFDNNYCRNPDDGQPRWC 240

QY 272 YTLDDHTRWECAITKCADNMTNDPDUPLTECTQOGOGEGYRGVTINTINGIPQRWDS 331
 Db 241 YTLDDHTRWECAITKCADNMTNDPDUPLTECTQOGOGEGYRGVTINTINGIPQRWDS 300

QY 332 OYPHEHDMPENFKDKLRENCRNPDDGQSPWCFTDPNIRVGYSQIOPNCMDMSHGDC 391
 Db 301 QYPHEHDMPENFKDKLRENCRNPDDGQSPWCFTDPNIRVGYSQIOPNCMDMSHGDC 360

QY 392 YRGNSKNYGMNLQSRSGLTCSMWNKMDMLRHFWEPDAKLNENYCRRNPDGQPRWC 451
 Db 421 CYTGMLPLPDYCPISRCEDTTPTIVNLUHPVISAKTQLRVNGIPTRNIGMVL 480

QY 361 YRGNSKNYGMNLQSRSGLTCSMWNKMDMLRHFWEPDAKLNENYCRRNPDGQPRWC 420

QY 452 CYTGMLPLPDYCPISRCEDTTPTIVNLUHPVISAKTQLRVNGIPTRNIGMVL 511
 Db 512 RYRNKHICGGSLIKSWSWLTAROCPSRSRDLKDYEAWLGIHDVHGDECKQVQLNWSOLV 571
 Db 481 RYRNKHICGGSLIKSWSWLTAROCPSRSRDLKDYEAWLGIHDVHGDECKQVQLNWSOLV 540

RESULT 12
 US-08-460-890A-50
 Sequence 50, Application US/08460890A
 Patent No. 5994109
 GENERAL INFORMATION:
 APPLICANT: Woo, Savi L.C.
 APPLICANT: Smith, Louis C.
 APPLICANT: Cristiano, Richard J.
 APPLICANT: Gottchalk, Stephen
 TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND
 NUMBER OF SEQUENCES: 65
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

RESULT 1³
US-08-167-641C-50
; Sequence 50, Application US/08167641C
; Patent No. 603884
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,641C
FILING DATE: December 14, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07,855,389
FILING DATE: March 20, 1992
APPLICATION NUMBER: PCM/US93/02725
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 205/012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 439-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 697 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
-US-08-167-641C-50

RESULT 1³
US-08-460-971A-50
; Sequence 50, Application US/08460971A
; Patent No. 6150168
GENERAL INFORMATION:
APPLICANT: Woo, Savio L.C.
APPLICANT: Smith, Louis C.
APPLICANT: Cristiano, Richard J.
APPLICANT: Gottchalk, Stephen
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:

Db 61 ARKOCILWFPNSMSSGVKEFGHEFDLYENKDYIRNCIIGKGRSYKGTVSITKGGIKOP 120
 Qy 152 WSSMPHENSPFLPSYRGKQLOQENYCRNPGEEGCPWCFSNPERYCDIPOCEVEC 211
 Db 121 WSSMPHENSPFLPSYRGKQLOQENYCRNPGEEGCPWCFSNPERYCDIPOCEVEC 180
 Qy 212 MTCNGESYRGLMDHESGKTCORMPHOTPHRKELPERYCDIPOCEVEC 271
 Db 181 MTCNGESYRGLMDHESGKTCORMPHOTPHRKELPERYCDIPOCEVEC 240
 Qy 272 YTLDPHTRWEYCAIKTCADNTMDNDTDPLETECGCQGQSGYRGTYNTIWNGIPQQRWDS 331
 Db 241 YTLDPHTRWEYCAIKTCADNTMDNDTDPLETECGCQGQSGYRGTYNTIWNGIPQQRWDS 300
 Qy 332 QYPHEHDIMTPENFKDOLRENYCRNPDGSESPWCFTTDPNTRVGCSQINCDSMHQDC 391
 Db 301 QYPHEHDIMTPENFKDOLRENYCRNPDGSESPWCFTTDPNTRVGCSQINCDSMHQDC 360
 Qy 392 YRGNGKNYMGNLSQLTRSGLTCMSWDKNMEDLRHFWEPDASKLENYCRNPDDBAHGPW 451
 ||||| YRGNGKNYMGNLSQLTRSGLTCMSWDKNMEDLRHFWEPDASKLENYCRNPDDBAHGPW 420
 452 CYTGNPPLIPWDYCPIISCGEGDTPTIVNLDHVISAKTKOLRVNGIPTETNIGNVSL 511
 ||||| CYTGNPPLIPWDYCPIISCGEGDTPTIVNLDHVISAKTKOLRVNGIPTETNIGNVSL 480
 Db 421 CYTGNPPLIPWDYCPIISCGEGDTPTIVNLDHVISAKTKOLRVNGIPTETNIGNVSL 480
 Qy 512 RYRNKHICGGSLIKEWSVLTARQCPSPRLKDVYEAMGIHVGREDECKOVLVNSQLV 571
 Db 481 RYRNKHICGGSLIKEWSVLTARQCPSPRLKDVYEAMGIHVGREDECKOVLVNSQLV 540
 Qy 572 YSPEGSDIVLMKLARPAVLDDEVSTIDLPNKGCTIPEKTSCEVYNGYTGLLINYDGLRV 631
 ||||| YSPEGSDIVLMKLARPAVLDDEVSTIDLPNKGCTIPEKTSCEVYNGYTGLLINYDGLRV 600
 Db 541 YGEGSDIVLMKLARPAVLDDEVSTIDLPNKGCTIPEKTSCEVYNGYTGLLINYDGLRV 600
 Qy 632 AHYIMGNEKCSOHHRGKVTLNESEICAGAEKIGSGPCEGDDYGGPLVCEQHKMRMVGLVI 691
 Db 601 AHLYIMGNEKCSOHHRGKVTLNESEICAGAEKIGSGPCEGDDYGGPLVCEQHKMRMVGLVI 660
 Qy 692 VPGRCALPNRPGIFVRVAYAKWIKHLITLYKPVOS 728
 ||||| VPGRCALPNRPGIFVRVAYAKWIKHLITLYKPVOS 697
 Db 661 VPGRCALPNRPGIFVRVAYAKWIKHLITLYKPVOS 697

Search completed: June 18, 2002, 17:47:21
 Job time: 242 sec